

LANL T-6 HIV Databases

HIV Immunology Web App

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Immunology API - API access for the LANL HIV Molecular Immunology Database

1.1 VERSION

This documentation refers to API version v2.2.1.

1.2 SYNOPSIS

```
wget -O- 'https://www.hiv.lanl.gov/mojo/immunology/api/v2/epitope/ctl?id=42'
```

1.3 DESCRIPTION

The HIV Immunology API provides a public interface to retrieve data from the LANL HIV Molecular Immunology database. The returned data are formatted as JSON.

1.4 ENDPOINTS

All endpoints are relative to the server installation path. For example, if the API is installed at *https://www.hiv.lanl.gov/mojo/immunology* , then the full path of /api/v2/epitope/ctl would be *https://www.hiv.lanl.gov/mojo/immunology/api/v2/epitope/ctl* .

The following endpoints are available:

/api/v2/epitope/{table}

Search {table} in the immunology database and return the matching epitope records.

Search parameters The {table} and at least one search parameter must be supplied; otherwise an error occurs. If multiple search parameters are supplied, then all of them must be satisfied.

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- **table**

One of `ctl`, `helper`, or `ab`. The HIV Molecular Immunology Database is organized into three main tables according to the immune response: CTL/CD8+ (`ctl`), T-helper/CD4+ (`helper`), and Antibodies (`ab`). The T-cell tables are `ctl` and `helper`; the antibody table is `ab`.

- **author**

Search for epitopes by the name of an author of a reference.

- **author_first author_last**

Restrict search by author to only first authors or only last authors respectively.

- **au_filter**

Filter the results to include only notes and references with the matching `author`. Requires `author`. Antibody only.

- **binding_type**

Search for epitopes by ID of the antibody binding type. See `"/api/v2/list/binding_type/{table}"` to obtain the list of binding types and IDs. Antibody only.

- **cite**

Search for epitopes by the citation key of a reference, *E.g.*, `Doe2008`.

- **dna_end**

Search for epitopes before this DNA location.

- **dna_start**

Search for epitopes after this DNA location.

`dna_start` and `dna_end` search for epitopes by DNA location. The epitope is matched if the contig overlaps `dna_start - dna_end`.

- **end**

Search for epitopes before this protein location; requires `protein` or `protein_name`. See also `start`.

`start` and `end` search for epitopes by protein location. The epitope is matched if the location overlaps `start - end`.

- **epitope**

Search for epitopes by epitope amino acid sequence. The match succeeds if the query sequence is in the epitope sequence. The wildcard characters `?` and `*` may be used to specify one or any number of arbitrary amino acids respectively.

- **epitope_exact**

Determines how the `epitope` parameter is matched against the database. The valid options for this parameter are:

- **embed**

Finds epitopes that contain the query sequence. Results will be the same length or longer than the query.

- **exact**

Finds epitopes with the exact coordinates and exact sequence as the query.

- **fuzzy**

Finds epitopes with the exact coordinates as the query, but with up to 25% difference in the amino acid sequence.

- **epitope_name**

Search for epitopes by name.

- **hla**

Search for epitopes by restricting MHC/HLA. T cell only.

- **hla_id**

Search for epitopes by restricting MHC/HLA ID. T cell only. See `"/api/v2/list/hla/{table}"` to obtain the list of HLAs and IDs.

- **id**

Search for epitopes by database ID.

- **immunogen**

Search for epitopes by immunogen ID. See `"/api/v2/list/immunogen/{table}"` to obtain the list of immunogens and IDs.

- **isotype**

Search for epitopes by isotype ID. See `"/api/v2/list/isotype/{table}"` to obtain the list of isotypes and IDs. Antibody only.

- **keyword**

Search for epitopes by keyword ID. See `"/api/v2/list/keyword/{table}"` to obtain the list of keywords and IDs.

- **kw_filter**

Filter the results to include only notes and references with the matching `keyword`. Requires `keyword`. Antibody only.

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- **mab_name**

Search for epitopes by the name (or alias) of the monoclonal antibody (mAb). Antibody only.

- **note**

Search for epitopes by the text in a note. The search is limited to a single word or phrase. Full-text search is not supported.

- **note_filter**

Filter the results to include only notes and references matching **note**. Requires **note**. Antibody only.

- **outcome**

Search for epitopes by outcome (experimental methods or outcomes measures) ID. See `"/api/v2/list/outcome/{table}"` to obtain the list of outcomes and IDs. T cell only.

- **protein**

Search for epitopes by protein ID. See `"/api/v2/list/protein/{table}"` to obtain the list of proteins and IDs.

- **protein_name**

Search for epitopes by protein name.

- **pubmed_id**

Search for epitopes by the PubMed ID of a reference.

- **range_span**

Determines how the **start** and **end** parameters are matched

- **Default**

This applies if neither **exact** nor **embed** is specified.

Finds epitopes that overlap any residue of the specified location. Results will be the same length or longer than the query. To find epitopes that contain a single specific residue, you can enter the same coordinate number for both **start** and **end**.

- **embed**

Finds epitopes that are contained within the specified range. Results will be the same length or shorter than the query.

- **exact**

Finds epitopes that have exactly the specified start and end coordinates. Results will be the same length as the query.

- **spans**

Search for epitopes at this protein location; requires `protein` or `protein_name`.

- **species**

Search for epitopes by the species ID the immune response was observed in. See `"/api/v2/list/species/{table}"` to obtain the list of species and IDs.

- **start**

Search for epitopes after this protein location; requires `protein` or `protein_name`. See also `end`.

- **subtype**

Search for epitopes by viral subtype ID. See `"/api/v2/list/subtype/{table}"` to obtain the list of subtypes and IDs.

- **vaccine_adjuvant**

Search for epitopes by vaccine adjuvant ID. Requires that the `immunogen` be a vaccine. See `"/api/v2/list/vaccine_adjuvant/{table}"` to obtain the list of vaccine adjuvants and IDs.

- **vaccine_component**

Search for epitopes by vaccine component ID. Requires that the `immunogen` be a vaccine. See `"/api/v2/list/vaccine_component/{table}"` to obtain the list of vaccine components and IDs.

- **vaccine_strain**

Search for epitopes by vaccine strain ID. Requires that the `immunogen` be a vaccine. See `"/api/v2/list/vaccine_strain/{table}"` to obtain the list of vaccine strains and IDs.

- **vaccine_type**

Search for epitopes by vaccine type ID. Requires that the `immunogen` be a vaccine. See `"/api/v2/list/vaccine_type/{table}"` to obtain the list of vaccine types and IDs.

`/api/v2/list/binding_type/{table}`

Retrieve the list of antibody binding types and IDs present in `{table}`. Antibody only.

`/api/v2/list/country/{table}`

Retrieve the list of country names and ISO country codes present in `{table}`.

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/api/v2/list/hla/{table}

Retrieve the list of restricting HLA/MHC types and IDs present in {table} . T cell only.

/api/v2/list/immunogen/{table}

Retrieve the list of immunogens and IDs present in {table} .

/api/v2/list/isotype/{table}

Retrieve the list of isotypes and IDs present in {table} . Antibody only.

/api/v2/list/keyword/{table}

Retrieve the list of keywords and IDs present in {table} .

/api/v2/list/outcome/{table}

Retrieve the list of outcomes (experimental methods and outcomes measured) and IDs present in {table} .

/api/v2/list/protein/{table}

Retrieve the list of proteins and IDs present in {table} .

/api/v2/list/species/{table}

Retrieve the list of species and IDs present in {table} .

/api/v2/list/subtype/{table}

Retrieve the list of subtypes and IDs present in {table} .

/api/v2/list/vaccine_adjuvant/{table}

Retrieve the list of vaccine adjuvants and IDs present in {table} .

/api/v2/list/vaccine_component/{table}

Retrieve the list of vaccine components and IDs present in {table} .

/api/v2/list/vaccine_strain/{table}

Retrieve the list of vaccine strains and IDs present in {table} .

/api/v2/list/vaccine_type/{table}

Retrieve the list of vaccine types and IDs present in {table} .

/api/v2/patient

Search the patient table in the immunology database and return the matching patient records.

Search parameters At least one search parameter must be supplied; otherwise an error occurs. If multiple search parameters are supplied, then all of them must be satisfied.

- **ethnicity**

Search for patients by ethnicity.

- **id**

Search for patients by database ID.

- **infection_country**

Search for patients by country where infected.

- **infection_year**

Search for patients by year when infected.

- **note**

Search for patients by the text in a note. The search is limited to a single word or phrase. Full-text search is not supported.

- **patient_code**

Search for patients by code as published in the literature.

- **patient_code_exact**

If true, find only exact matches to `patient_code`.

- **patient_hla_id**

Search for patients by MHC/HLA ID.

- **patient_sex**

Search for patients by sex.

- **progression**

Search for patients by HIV progression status.

- **risk_factor**

Search for patients by HIV risk factor.

- **species**

Search for patients by species.

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/api/v2/patient_list/ethnicity

Retrieve the list of patient ethnicities.

/api/v2/patient_list/hla

Retrieve the list of patient HLA/MHC types and IDs.

/api/v2/patient_list/infection_country

Retrieve the list patient infection country names and codes.

/api/v2/patient_list/infection_year

Retrieve the list of patient infection years.

/api/v2/patient_list/progression

Retrieve the list patient HIV progression codes and names.

/api/v2/patient_list/risk_factor

Retrieve the list patient HIV risk factor codes and names.

/api/v2/patient_list/sex

Retrieve the list patient sexes.

/api/v2/patient_list/species

Retrieve the list patient species.

/api/v2/variant/{table}

Search parameters The {table} and at least one search parameter must be supplied; otherwise an error occurs. If multiple search parameters are supplied, then all of them must be satisfied.

- **table**

One of `ctl` or `helper`. These are the tables that contain epitope variant data.

- **cite**

Search for epitopes by the citation key of a reference, *E.g., Doe2008*.

- **end**

Search for epitopes before this protein location; requires `protein` or `protein_name`. See also `start`.

start and **end** search for epitopes by protein location. The epitope is matched if the location overlaps **start –end**.

- **epitope**

Search for epitopes by epitope or variant amino acid sequence. The match succeeds if the query sequence is in the epitope sequence. The wildcard characters ? and * may be used to specify one or any number of arbitrary amino acids respectively.

- **epitope_exact**

Determines how the **epitope** parameter is matched against the database. The valid options for this parameter are:

- **embed**

Finds epitopes that contain the query sequence. Results will be the same length or longer than the query.

- **exact**

Finds epitopes with the exact coordinates and exact sequence as the query.

- **fuzzy**

Finds epitopes with the exact coordinates as the query, but with up to 25% difference in the amino acid sequence.

- **epitope_id**

Search for epitopes by database ID.

- **hla_id**

Search for epitopes by restricting MHC/HLA ID. T cell only. See ["/api/v2/list/hla/{table}"](#) to obtain the list of HLAs and IDs.

- **mutation_type_filter**

Filter the results to include only variants with the matching **mutation_type_id**.

- **mutation_type_id**

Search for epitopes with variants matching mutation type ID.

- **protein**

Search for epitopes by protein ID. See ["/api/v2/list/protein/{table}"](#) to obtain the list of proteins and IDs.

- **protein_name**

Search for epitopes by protein name.

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- **range_span**

Determines how the `start` and `end` parameters are matched

- **Default**

This applies if neither `exact` nor `embed` is specified.

Finds epitopes that overlap any residue of the specified location. Results will be the same length or longer than the query. To find epitopes that contain a single specific residue, you can enter the same coordinate number for both `start` and `end`.

- **embed**

Finds epitopes that are contained within the specified range. Results will be the same length or shorter than the query.

- **exact**

Finds epitopes that have exactly the specified start and end coordinates. Results will be the same length as the query.

- **spans**

Search for epitopes at this protein location; requires `protein` or `protein_name`.

- **start**

Search for epitopes after this protein location; requires `protein` or `protein_name`. See also `end`.

- **variant_id**

Search for epitopes with the matching variant ID.

- **variant_id_filter**

Filter the results to include only variants with the matching `variant_id`.

- **variant_method_filter**

Filter the results to include only variants with the matching `variant_method_id`.

- **variant_method_id**

Search for epitopes with variants matching variant method ID.

`/api/v2/variant_list/hla/{table}`

Retrieve the list of restricting HLA/MHC types and IDs present in `{table}`. The list is restricted to HLA types of epitopes with variants.

`/api/v2/variant_list/method/{table}`

Retrieve the list of variant methods and IDs present in `{table}`.

`/api/v2/variant_list/mutation_type/{table}`

Retrieve the list of variant mutation types and IDs present in `{table}`.

`/api/v2/variant_list/protein/{table}`

Retrieve the list of proteins and IDs present in `{table}`. The list is restricted to proteins with epitopes with variants.

1.5 DATABASE ORGANIZATION

The information below explains what the database contains and the meaning of terms used in the search interfaces.

HIV T-Cell Epitopes

T-cell epitopes are categorized into cytotoxic T lymphocytes (CTL/CD8+) and helper T lymphocytes (T-helper/CD4+). The database organization for CTL/CD8+ and T-helper/CD4+ is identical, so they are described together.

T cell summary The T cell databases include tables and associated references of HIV-specific T-cell epitopes arranged according to the location of the proteins in the HIV-1 genome. We attempted to make this section as comprehensive as possible, requiring that the epitope be contained within a defined region of a maximum of 30 amino acids, but not that the optimal boundaries be defined. Studies that were based on the analysis of whole proteins are described at the end of each protein section. The same epitope can have multiple entries, and each entry represents a single publication in this section of the database.

Recent studies utilize multiple functions attributed to T cells to define responses, and the simple distinctions of cytotoxic T cells and helper T cells have become blurred as more is learned about the range of responses triggered in CD4- and CD8-positive T cells responding to antigenic stimulus. When adding the most recent studies, we have tried to place T-cell responses in a reasonable manner into our traditional CTL and helper T-cell sections, and to specify the assay used to measure the response in each study.

T cell epitope tables Each T cell epitope has a multi-part basic entry:

- **Record number**

A unique number assigned by the database, in approximate order of entry. Please refer to this number if you have any comments or questions about an entry.

- **HXB2 Location**

The viral strain HXB2 (GenBank Accession Number K03455) is used as a reference strain throughout this publication. The position of the defined epitope location relative to the sequence of the HXB2 protein is indicated. The numbering in this table corresponds to the protein maps. Because of HIV-1 variation the epitope may not actually be present in HXB2, rather the position in HXB2 indicates the position aligned to the epitope. HXB2 was selected as the reference strain because so many studies use HXB2, and because crystal structures for HXB2-related proteins are available.

Occasionally, an unusual epitope sequence will not have a location entry if, for instance, it is cryptic, junction, or a SIV sequence.

- **Author Location**

The amino acid positions of the epitope boundaries and the reference sequence are listed as given in the primary publication. Frequently, these positions as published are imprecise, and do not truly correspond to the numbering of the sequence, but they provide a reasonable guide to the peptide's approximate location in the protein. Also, in many cases the reference sequence identification was not provided, and in such cases it is not possible to use these numbers to specify precise locations.

- **Subtype**

The subtype under study, generally not specified for B subtype.

- **Epitope Sequence**

The amino acid sequence of the epitope of interest as defined in the reference. On occasions when only the position numbers and not the actual peptide sequence was specified in the original publication, we try to fill in the peptide sequence based on the position numbers and reference strain. If the sequences were numbered inaccurately by the primary authors, or if we made a mistake in this process, we may misrepresent the amino acid sequence. Because of this uncertainty, epitopes that were not explicitly written in the primary publication are followed by a question mark (?) in the table.

- **Epitope Name**

If the epitope has a name attributed by the publication, it is recorded here, *e.g.* "SL9".

- **Species (MHC/HLA)**

The species responding and MHC or HLA specificity of the epitope.

- **Immunogen**

The original stimulus of the T-cell response. Often this is an HIV-1 infection. If a vaccine was used as the original antigenic stimulation, not a natural infection, this is noted on a separate line, and additional information about the vaccine antigen is provided as available.

- **Keywords**

The keyword field helps identify entries of particular interest.

- **Reference**

The primary reference (sometimes two or more directly related studies are included).

- **Notes**

Brief comments explain the context in which the epitope was studied and what was learned about the epitope in a given study.

HIV Antibody Binding Sites

Anibody summary The antibody database summarizes HIV-specific antibodies (Abs) arranged sequentially according to the location of their binding domain, organized by protein. We attempted to make this section as comprehensive as possible. For the monoclonal (MAbs) capable of binding to linear peptides, we require that the binding site be contained within a region of 30 or so amino acids to define the epitope, but not that the precise boundaries be defined. MAbs that do not bind to defined linear peptides are grouped by category at the end of each protein. Antibody categories, for example CD4 binding site (CD4BS) antibodies, are also noted in the index at the beginning of this section. Studies of polyclonal Ab responses are also included. Responses that are just characterized by binding to a protein, with no known specific binding site, are listed at the end of each protein.

Antibody tables Each MAb or polyclonal response has a multi-part basic entry:

- **Record number**

A unique number assigned by the database, in approximate order of entry. Please refer to this number if you have any comments or questions about an entry.

- **MAb name**

The name of the monoclonal antibody with synonyms in parentheses. MAbs often have several names. For example, punctuation can be lost and names are often shortened (“M-70” in one paper can be “M70” in another). Polyclonal responses are listed as “polyclonal” in this field.

- **HXB2 Location**

Position of the Ab binding site relative to the viral strain HXB2 (Gen-Bank Accession Number K03455), which is used as a reference strain throughout this publication. The numbering in this table corresponds to the protein maps. Because of HIV-1 variation the epitope may not actually be present in HXB2, rather the position in HXB2 indicates the position aligned to the epitope. HXB2 was selected as the reference strain because so many studies use HXB2, and because crystal structures for HXB2-related proteins are often available.

- **Author Location**

The amino acid positions of the epitope boundaries and the reference sequence used to define the epitope are listed as given in the primary publication. Frequently, these positions as published are imprecise, and do not truly correspond to the numbering of the sequence, but they provide a reasonable guide to the peptide’s approximate location in the protein. Also, in many cases, position numbers were provided but the reference sequence identification was not. Because of HIV-1’s variability, position numbers require a reference strain to be meaningful. Binding sites that cannot be defined through peptide binding or interference studies are labeled as discontinuous. The approximate location on the protein, sequence number, and reference sequence are listed.

- **Sequence**

The amino acid sequence of the binding region of interest, based on the reference strain used in the study defining the binding site. On occasions when only the position numbers and not the actual peptide sequence was specified in the original publication, we tried to fill in the peptide sequence based on the position numbers and reference strain. If the sequences were numbered inaccurately by the primary authors, or if we made a mistake in this process, we may have misrepresented the binding site’s amino acid sequence. Because of this uncertainty, epitopes that were not explicitly written in the primary publication, that we determined by looking up the reference strain and the numbered location, are followed by a question mark in the table.

- **Neutralizing**

- *L* : neutralizes lab strains.
- *P* : neutralizes at least some primary isolates or pseudoviruses.
- *P (tier 1)* : neutralizes tier 1 isolates (easily neutralized strains).
- *P (tier 2)* : neutralizes at least some tier 2 isolates (moderately difficult strains).
- *no* : does not neutralize.

No information in this field means that neutralization was either not discussed or unresolved in the primary publications referring to the MAb.

- **Immunogen**

The antigenic stimulus of the original B cell response. Often this is an HIV-1 infection. If a vaccine was used as the original antigenic stimulation, not a natural infection, this is noted on a separate line, and additional information about the vaccine antigen is provided as available.

- **Species(Isotype)**

The host that the antibody was generated in, and the isotype of the antibody.

- **Donor**

Information about an antibody or how to obtain it, as well as to provide credit.

- **References**

All publications that we could find that refer to the use of a specific monoclonal antibody. First is a list of all references. Some of the earlier references include notes with additional details, although we have tried to keep the entries self-contained since 1997.

- **Notes**

Describe the context of each study, and what was learned about the antibody in the study.

Database Fields

This is a brief description of the database fields in the search and results pages. Please see above for more details.

- **HIV protein**

The protein for which the epitope was defined.

- **Defined epitopes**

Epitopes or reactive peptides that have a known protein sequence.

- **Undefined epitopes**

Reactive peptides or proteins for which the binding site is not exactly known. This could either be because it was unspecified by the authors (e.g., a polyclonal response to Env) or because it is a conformational epitope for an antibody that binds to discontinuous amino acids in the folded protein.

- **HXB2 protein location**

The HXB2 protein coordinates within the protein selected in the “HIV protein” field above. Be sure to enter a HIV protein when using protein location search. This finds epitopes that overlap any residue of the specified location. To find epitopes that contain a single specific residue, you can enter the same coordinate number in both boxes.

- **HXB2 DNA location**

The HXB2 DNA coordinates. Results will include all epitopes that overlap the coordinates of the query. If multiple proteins overlap at the DNA coordinates selected, you can use the “HIV protein” field to narrow the search to the protein of interest.

- **Epitope**

The amino acid sequence of the epitope or short reactive peptide. Finds epitopes that contain the query sequence. Results will be the same length or longer than the query.

- **Epitope name**

Epitope name as reported by the authors.

- **Record number**

A unique number assigned by the database, in approximate order of entry. Please refer to this number if you have any comments or questions about an entry.

- **Subtype**

The subtype under study, generally not specified for B subtype.

- **Immunogen**

The stimulus of the original immune response under study.

- **Vaccine details**

Data included only if the immunogen was a vaccine.

- **Vaccine type**

The vaccine construct and boost.

- **Vaccine strain**

The strain of HIV or SHIV used for the vaccine antigen.

- **Vaccine component**

The HIV protein (complete or partial) included in the vaccine.

- **Adjuvant**

Traditional adjuvants or chemokines.

- **Species**

The species in which the immune response was stimulated.

- **Restricting MHC/HLA**

The MHC (or HLA) presenting molecules as described by the primary authors.

- **Author**

Any one author from primary publication. Specify as surname and initials, *e.g.* , “Brander C”, “Korber BT” or “Haynes”.

- **Country**

The country where the samples were obtained.

- **Keywords**

Searchable topics that can be used to narrow your search. Each reference is assigned one or more keywords that characterize the information provided in that paper.

- **Experimental methods (outcome)**

Methods used by the authors to test the immune response.

- **MAb name**

Name of monoclonal antibody or “polyclonal” if a general response is being studied. The name is usually given as the authors defined it in the paper that described the antibody’s isolation.

- **HXB2 location**

Epitope position numbers in the HXB2 reference strain.

- **Author location**

Epitope location as reported by the authors. Includes strain and subtype from which the epitope was derived.

- **Epitope name**

Epitope name as reported by the authors.

- **Ab binding type**

Classes of antibodies have shared properties with regard to their binding site and can be grouped; for example they might bind to a similar region (like V3) or near a common functional domain (like the CD4 binding site, CD4BS).

- **Neutralizing**

Neutralizing properties of the antibody—often different studies involving the same antibody will report this differently, so this classification is somewhat subjective.

- **Research contact (donor)**

The person or lab that generated or provides the antibody.

- **Notes**

Brief comments explain the context in which the epitope was studied and what was learned about the epitope in a given study.

Epitope Variants

The variant tables contain information about sequence variants and mutations of HIV-1 T-cell epitopes. Variants tested for immunological response as well as those observed in longitudinal intra-patient, subtype comparison, or other inter-patient studies are included. Variants are usually annotated even if the paper only provides sequence or statistical data, this is different from epitope annotations where only immunogenic epitopes or peptides are annotated. Each variant record is attached to one epitope record; an epitope record may have zero, one, or more variants.

General information about the HIV immunology database and searches is described above.

Epitope variant search and results fields This is a brief description of the database fields in the variant search and results pages.

- **HIV protein**

The protein for which the epitope was defined.

- **HXB2 protein location**

The HXB2 protein coordinates within the protein selected in the “HIV protein” field above. Three options determine the type of search:

- *Results overlap with query location:* finds epitopes that overlap any residue of the specified location. To find epitopes that contain a single specific residue, you can enter the same coordinate number in both boxes.

- *Results contained within query location:* finds epitopes that are contained within the specified range. Results will be the same length or shorter than the query.
- *Results exact match to query location:* finds epitopes that have exactly the specified start and stop coordinates.

- **Epitope or variant sequence**

The amino acid sequence of the epitope or variant. Three options determine the type of search:

- *Results contain query sequence:* finds epitopes that contain the query sequence. Results will be the same length or longer than the query.
- *Results exact match to query sequence:* finds epitopes with the exact sequence as the query.
- *Results fuzzy match to query sequence:* finds epitopes with up to 25% difference in the amino acid sequence.

- **Epitope record number**

A unique number assigned to an epitope by the database. Please refer to this number if you have any comments or questions about an entry.

- **Variant record number**

A unique number assigned to a variant by the database. Please refer to this number if you have any comments or questions about an entry.

- **Mutation type**

Mutations are classified into various types, depending on the evidence presented in the paper. Assigning the mutation type is sometimes a subjective judgement of the annotator; it is not always clear in the paper. Read the notes for the variant carefully, and refer to the original paper if necessary.

- **Restricting MHC/HLA**

The MHC (or HLA) presenting molecules as described by the primary authors.

- **Variant method**

The method(s) used to ascertain the type of mutant.

- **Note**

In the note for the variant, the annotator explains the evidence for assigning the mutation type.

- **HXB2 location**

Epitope position numbers in the HXB2 reference strain.

- **Epitope name**

Epitope name as reported by the authors.

- **Epitope**

The amino acid sequence of the epitope or short reactive peptide.

- **Epitope sequence**

The amino acid sequence of the HIV immunogenic epitope or short reactive peptide. There is a limit of 30 amino acids for peptides. This is also the “index” epitope sequence mentioned in further definitions on this page.

- **Variant sequence**

The amino acid sequence of the variant (mutated epitope sequence in reference to the index epitope or short reactive peptide).

- **Mutations**

The insertion or absence or change of an amino acid in HIV protein sequence, most often studied in or around epitopes for the purposes of this database.

- **Epitope mutation location**

The position of the mutation within or in reference to the epitope, and the “from” and “to” amino acid values. For example: the mutations in variant sequence RSLYNT*i*AvLY , in reference to index epitope RSLYNTVATLY , are shown as V7I T9V [“from” AA, location, “to” AA]. Insertions have the form (X.Y) where X is the epitope location/position just before the insertion, and Y is the insertion number. For example, if ss is inserted between epitope positions 4 and 5, then the position of the first inserted s would be (4.1) and the location of the second inserted s would be (4.2). Positions/locations in the left flank (upstream insertions) have a prefix of minus. For example, the a in variant {a**}KkWIILGLNK has position -3. Locations in the right flank have a prefix of '+'. For example, the t in variant KIRLRPGGK{*t} is position +2. Insertions in the right flank (downstream insertions) have the form (+X.Y) while insertions in the left flank have the form (-X.Y). Flanking sequences are enclosed in curly braces. Asterisks in flanking sequences indicate an unpublished AA, but correspond one-to-one to AAs.

- **HXB2 mutation location**

The position/location of the mutation within or in reference to the protein (HXB2 reference sequence used) it is in and the “from” and “to” values, for example: L64V. Multiple values are separated with by spaces, for example: L64V I72T. Insertions have the form (X.Y) were X is the protein position/location just before the insertion, and Y is the insertion number. For example, if ss is inserted between protein positions 193 and 194, then the position of the first inserted s would be (193.1) and the position of the second inserted s would be (193.2). Variant positions in the left or right flanks (i.e upstream or downstream regions) are derived by subtracting (or adding) from the beginning (or ending) of the HXB2 position. For example: the mutations in variant sequence RSLYNT*i*AvLY , in reference to index epitope RSLYNTVATLY and located within Gag, are shown as V82I T84V [“from” AA, location, “to” AA]. Also, the protein position for the r in variant {r*}QVPLRPMTYK is 188 because the beginning HXB2 location for the epitope is 190. Similarly the protein position for the g in variant QVPLRPMTYK{g} is 200, since the HXB2 ending position for the epitope is 199. Flanking sequences are enclosed in curly brackets. Asterisks in flanking sequences indicate an unpublished AA, but correspond one-to-one to AAs. Locations in the left flank have a prefix of minus.

- **Epitope subtype**

The subtype of HIV in which the index epitope sequence or immunogenic peptide under study is found, sometimes not specified for B subtype.

- **Variant subtype**

The subtype of HIV in which the variant sequence under study is found, sometimes not specified for B subtype.

Patient Data

Description The patient tables contain information about individual subjects from whom biological samples have been acquired for immunological study related to HIV infection. Patients primarily tested for immunological response are included. Patients also may be included if they are listed in the paper as part of a cohort under study, even if their immunological response has not been annotated. Generally, each patient record is attached to one or more epitope records and each epitope record has zero, one, or more records associated with it.

Depending on the publication, patients may also be called participants, subjects, volunteers, individuals or donors.

Patient Search and Results Fields This is a brief description of the database fields in the patient search form and results pages.

- **Patient code**

The name or label by which the subject under study is referred to. Spaces are allowed and the code name used is according to what the author published. Alias names from other publications can also be searched here. An option for the search is to query for an exact match by checking the box.

- **Patient record number**

This is the patient record number, which is distinct from the associated CTL epitope, Helper/HTL epitope, or Ab record number. Each individual patient record is assigned a unique patient record number and can be searched for using the patient record number.

- **Patient MHC/HLA**

The patient's known HLAs as given in the paper, whether determined by serotype or genotype and including MHC Class I as well as MHC Class II molecules. The HLA Informatics Group's current nomenclature is followed and obsolete nomenclature has been updated to current within all fields except for "Note". Users may still search for obsolete HLA nomenclature within the note section of the patient search. The annotated note in the patient tables use the author's terminology for HLA from the paper.

- **Patient sex**

'Male' / 'Female' / 'Other': the patient's biological sex. 'Other' may be more clearly explained in the notes section for an individual patient.

- **Risk factor**

This is the primary route by which the patient acquired infection. If there is more than one route of infection acquisition, it will be mentioned in the note section.

- **Infection country**

The country where the patient became infected with HIV, if known (not necessarily their country of origin, domicile, or sampling).

- **Infection city**

The city or town in which the patient acquired HIV infection (not necessarily the city in which they were sampled).

- **Infection year**

This is the year in which the patient acquired HIV infection, if known (not the year in which they were diagnosed).

- **Species**

Usually this is *homo sapien* /human, but other experimental animals may also be annotated.

- **Ethnicity**

This is the patient's race, nationality or sometimes their ethnic background or both. It is stated as given by authors in the paper.

- **Progression**

This is the author-defined rate of disease progression in the Patient sampled at the time of the study. Possible options are listed below, along with sample definitions from literature.

- *Controller or HIV Controller (HIC)*

HIC are a subset of LTNP who additionally have undetectable viraemia. Viral load (VL) undetectable. Mandalia et al. (2012) <https://doi.org/10.1371/journal.pone.0029844>

Typical controllers had an average recent CD4 cell count more than 450 cells/ l, whereas discord controllers had an average recent CD4 cell count less than 450 cells/ l. Sabin and Lundgren (2013). https://journals.lww.com/co-hivandaids/fulltext/2013/07000/the_natural_history_of_hiv_infection.10.aspx

- *Elite Controller (EC) or Natural Controller or Viral Controller*

Viral load < 200 RNA copies/ml. An EC may not reach LTNP status for years. This group, sometimes showing plasma HIV-RNA values persistently below 50 copies/ml, is termed "elite" or "natural controllers". Kumar, P.(2013) <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC3818590/>

ECs were defined as ART-naive patients infected with HIV for more than 12 months with at least three longitudinal undetectable HIV RNA determinations. Sabin and Lundgren (2013) https://journals.lww.com/co-hivandaids/fulltext/2013/07000/the_natural_history_of_hiv_infection.10.aspx

- *Elite Neutralizer (EN)*

A patient with Abs that neutralize their autologous HIV. These highest levels of bNAbs are found in the sera of rare individuals termed elite neutralizers (ENs). ENs are defined as HIV-1 infected individuals who possess antibodies capable of neutralizing tier 2

and 3 viruses from at least four different clades of virus at serum dilution titers of 1:300 or more. Mesa et al. (2019). <https://journals.plos.org/plosone/article?id=10.1371/journal.pone.0213409>

- *Long Term Non-Progressor (LTNP) or Long-term Slow-Progressor (LTSP)*

LTNP are HIV-1+ patients who maintain stable CD4+ T-cell counts, with no history of opportunistic infection or antiretroviral therapy (ART). Mandalia et al. (2012) <https://doi.org/10.1371/journal.pone.0029844>

The group of HIV positive long term non-progressors comprises less than 5% of the total HIV population. They also maintain low detectable plasma viraemia (<5000 HIV-RNA copies/ml). Kumar, P. (2013). ["/www.ncbi.nlm.nih.gov/pmc/articles/PMC3818590/"](https://www.ncbi.nlm.nih.gov/pmc/articles/PMC3818590/) in "<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC3818590/>"

Viral load does not change for more than 12 years.

<https://i-base.info/long-term-non-progressor-ltnp/>

- *Progressor (P)*

HIV positive patient who needs to take ART in order to control infection. Sabin and Lundgren (2013), https://journals.lww.com/co-hivandaids/fulltext/2013/07000/the_natural_history_of_hiv_infection.10.aspx https://journals.lww.com/co-hivandaids/fulltext/2013/07000/the_natural_history_of_hiv_infection.10.aspx

- *Rapid Progressor (RP)*

Rapid progression is when AIDS develops within 3 years of infection. Kumar, P. (2013). <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC3818590/>

- *Slow Progressor (SP)*

People who stay stable for a long time after infection are referred to as ‘slow progressors’. The definition of a slow progressor varies in different settings. A general definition though includes still having a CD4 count about 500 after five years and without using treatment. <https://i-base.info/qa/7831>

- **Note**

Any patient-specific information that is not included in the search fields above and that is mentioned in the paper being annotated. Information that changes with time for example age, CD4 count, days post-infection, plasma viral load (pVL) etc. are tied to either a specific epitope or antibody, publication, or sampling year.

- **Antibody records**

Antibody record is a unique record number for a specific antibody in the LANL HIV Immunology Database. The antibody(ies) linked to

the patient were derived from this patient's blood, or were synthesized from antibody sequences derived from this patient. Some synthetic antibodies may be derived from protein sequences originating from more than one patient, and thus may be linked to two or more patients. Please note that antibody record numbers and patient record numbers are distinct and from separate database tables.

- **CTL/CD8+ records**

CTL/CD8+ record refers to a unique record number for a specific cytotoxic T-lymphocyte epitope in the LANL HIV Immunology Database. The CTL records associated with a specific patient are those epitopes to which this patient had an immunological response. More than one patient may be linked to a single epitope and one patient may be linked to several epitopes if they had a response to all those epitopes. Please note that CTL/CD8+ record numbers and patient record numbers are distinct and from separate database tables.

- **T-Helper/CD4+ records**

T-helper (HTL)/CD4+ record refers to a unique record number for a specific helper T-lymphocyte epitope in the LANL HIV Immunology Database. The T-helper (HTL) records associated with specific patient are those epitopes to which this patient had an immunological response. More than one patient may be linked to a single HTL epitope and one patient may be linked to several HTL epitopes if they had a response to all those epitopes. Please note that T-helper (HTL)/CD4+ record numbers and patient record numbers are distinct and from separate database tables.

- **Sequence database patient record**

Some patients are annotated in both the LANL HIV Immunology database and the LANL HIV Sequence database. The two databases are independent and assign different record numbers. The sequence database patient ID provided here is a link to the same unique patient in the other database. From there, you can obtain all the HIV sequences associated with this patient.

1.6 API REFERENCE

The formal OpenAPI specification for this API is available via "`api/v2`" , E.g. , <https://www.hiv.lanl.gov/mojo/immunology/api/v2> . An HTML rendering is available via "`api/v2.html`" , E.g. , <https://www.hiv.lanl.gov/mojo/immunology/api/v2.html> .

1.7 BUGS AND LIMITATIONS

There are no known bugs in this app. Please report problems to the author at <mailto:immuno@lanl.gov>

1.8 SEE ALSO

HIV Molecular Immunology website <https://www.hiv.lanl.gov/content/immunology>

Immunology

OpenAPI/Swagger <https://swagger.io>

1.9 AUTHOR

LANL T-6 HIV Databases <mailto:immuno@lanl.gov>

1.10 LICENSE AND COPYRIGHT

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A OpenAPI Specification

openapi.json

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        "$ref": "#/components/schemas/IdType"
    }
},
"required": [
    "keyword_id",
    "keyword"
],
"type": "object"
},
"NoteRecord": {
    "description": "Record describing a note",
    "properties": {
        "cite": {
            "description": "Ab only",
            "items": {
                "type": "string"
            },
            "type": "array"
        },
        "keyword": {
            "description": "Ab only",
            "items": {
                "$ref": "#/components/schemas/KeywordRecord"
            },
            "type": "array"
        },
        "note": {
            "type": "string"
        },
        "note_no": {
            "minimum": 0,
            "type": "integer"
        }
},
"required": [
    "note",
    "note_no"
],
"type": "object"
}
```

```

    },
  "OutcomeRecord": {
    "properties": {
      "outcome": {
        "type": "string"
      },
      "outcome_id": {
        "$ref": "#/components/schemas/IdType"
      }
    },
    "required": [
      "outcome_id",
      "outcome"
    ],
    "type": "object"
  },
  "PatientEthnicityRecord": {
    "type": "string"
  },
  "PatientHLARecord": {
    "properties": {
      "hla": {
        "type": "string"
      },
      "hla_id": {
        "$ref": "#/components/schemas/IdType"
      }
    },
    "required": [
      "hla_id",
      "hla"
    ],
    "type": "object"
  },
  "PatientInfectionCountryRecord": {
    "properties": {
      "code": {
        "description": "2 character ISO country code",
        "maxLength": 2,
        "minLength": 2,
        "type": "string"
      },
      "name": {
        "description": "Country name",
      }
    }
  }
}

```

```

        "type": "string"
    },
},
"required": [
    "code",
    "name"
],
"type": "object"
},
"PatientInfectionYearRecord": {
    "type": "integer"
},
"PatientProgressionRecord": {
    "properties": {
        "progression_code": {
            "description": "HIV progression code",
            "maxLength": 6,
            "minLength": 1,
            "type": "string"
        },
        "progression_name": {
            "description": "HIV progression name",
            "type": "string"
        }
    },
    "required": [
        "progression_code",
        "progression_name"
    ],
    "type": "object"
},
"PatientRecord": {
    "description": "Record describing a patient",
    "properties": {
        "ab_epitopes": {
            "description": "Ab IDs and names",
            "items": {
                "properties": {
                    "id": {
                        "$ref": "#/components/schemas/IdType"
                    },
                    "mab_name": {
                        "type": "string"
                    }
                }
            }
        }
    }
}

```

```

        },
        "type": "object"
    },
    "type": "array"
},
"aliases": {
    "items": {
        "type": "string"
    },
    "type": "array"
},
"code": {
    "nullable": true,
    "type": "string"
},
"ctl_ids": {
    "description": "CD8/CTL IDs",
    "items": {
        "$ref": "#/components/schemas/IdType"
    },
    "type": "array"
},
"ethnicity": {
    "nullable": true,
    "type": "string"
},
"helper_ids": {
    "description": "CD4/T-helper IDs",
    "items": {
        "$ref": "#/components/schemas/IdType"
    },
    "type": "array"
},
"hla": {
    "items": {
        "type": "string"
    },
    "type": "array"
},
"infection_city": {
    "nullable": true,
    "type": "string"
},
"infection_country": {

```

741

751

761

771

```
    "maxLength": 2,
    "minLength": 2,
    "nullable": true,
    "type": "string"
},
"infection_country_name": {
    "nullable": true,
    "type": "string"
},
"infection_year": {
    "maximum": 2100,
    "minimum": 1967,
    "nullable": true,
    "type": "integer"
},
"infection_year_upper": {
    "maximum": 2100,
    "minimum": 1967,
    "nullable": true,
    "type": "integer"
},
"note": {
    "nullable": true,
    "type": "string"
},
"patient_id": {
    "$ref": "#/components/schemas/IdType"
},
"progression_code": {
    "nullable": true,
    "type": "string"
},
"progression_name": {
    "nullable": true,
    "type": "string"
},
"risk_factor_code": {
    "nullable": true,
    "type": "string"
},
"risk_factor_name": {
    "nullable": true,
    "type": "string"
}
```

```

    "seqdb_pat_id": {
        "minimum": 1,
        "nullable": true,
        "type": "integer"
    },
    "sex": {
        "nullable": true,
        "type": "string"
    },
    "species": {
        "nullable": true,
        "type": "string"
    },
    "species_id": {
        "minimum": 1,
        "nullable": true,
        "type": "integer"
    }
},
"required": [
    "patient_id"
],
"type": "object"
},
"PatientResponse": {
    "properties": {
        "error": {
            "description": "Error messages",
            "items": {
                "type": "string"
            },
            "type": "array"
        },
        "params": {
            "description": "Valid input parameters",
            "type": "object"
        },
        "patients": {
            "description": "List of matching patient records",
            "items": {
                "$ref": "#/components/schemas/PatientRecord"
            },
            "type": "array"
        }
}

```

831

841

851

861

```
        "timestamp": {
            "$ref": "#/components/schemas/TimeStamp"
        }
    },
    "required": [
        "patients",
        "params",
        "timestamp"
    ],
    "type": "object"
},
"PatientRiskFactorRecord": {
    "properties": {
        "progresssion_name": {
            "description": "HIV risk_factor name",
            "type": "string"
        },
        "risk_factor_code": {
            "description": "HIV risk_factor code",
            "maxLength": 6,
            "minLength": 1,
            "type": "string"
        }
    },
    "required": [
        "risk_factor_code",
        "risk_factor_name"
    ],
    "type": "object"
},
"PatientSexRecord": {
    "maxLength": 9,
    "minLength": 1,
    "type": "string"
},
"PatientSpeciesRecord": {
    "properties": {
        "species": {
            "type": "string"
        },
        "species_id": {
            "$ref": "#/components/schemas/IdType"
        }
    },
}
```

```

    "required": [
      "species_id",
      "species"
    ],
    "type": "object"
  },
  "ProteinRecord": {
    "properties": {
      "protein": {
        "type": "string"
      },
      "protein_id": {
        "$ref": "#/components/schemas/IdType"
      }
    },
    "required": [
      "protein_id",
      "protein"
    ],
    "type": "object"
  },
  "SpeciesRecord": {
    "properties": {
      "species": {
        "type": "string"
      },
      "species_id": {
        "$ref": "#/components/schemas/IdType"
      }
    },
    "required": [
      "species_id",
      "species"
    ],
    "type": "object"
  },
  "SubtypeRecord": {
    "properties": {
      "subtype": {
        "type": "string"
      },
      "subtype_id": {
        "$ref": "#/components/schemas/IdType"
      }
    }
  }
}

```

```

},
"required": [
  "subtype_id",
  "subtype"
],
"type": "object"
},
961 "TCellTable": {
  "description": "The main immunology tables for T-cell epitopes",
  "enum": [
    "ctl",
    "helper"
  ],
  "type": "string"
},
"Table": {
  "description": "The main immunology tables",
  "enum": [
    "ab",
    "ctl",
    "helper"
  ],
  "type": "string"
},
971 "TimeStamp": {
  "description": "When the results were generated",
  "format": "date-time",
  "type": "string"
},
"VaccineAdjuvantRecord": {
  "properties": {
    "vaccine_adjuvant": {
      "type": "string"
    },
    "vaccine_adjuvant_id": {
      "$ref": "#/components/schemas/IdType"
    }
  },
  "required": [
    "vaccine_adjuvant_id",
    "vaccine_adjuvant"
  ],
  "type": "object"
},
991

```

```

"VaccineComponentRecord": {
  "properties": {
    "vaccine_component": {
      "type": "string"
    },
    "vaccine_component_id": {
      "$ref": "#/components/schemas/IdType"
    }
  },
  "required": [
    "vaccine_component_id",
    "vaccine_component"
  ],
  "type": "object"
},
1011
"VaccineStrainRecord": {
  "properties": {
    "vaccine_strain": {
      "type": "string"
    },
    "vaccine_strain_id": {
      "$ref": "#/components/schemas/IdType"
    }
  },
  "required": [
    "vaccine_strain_id",
    "vaccine_strain"
  ],
  "type": "object"
},
1021
"VaccineTypeRecord": {
  "properties": {
    "vaccine_type": {
      "type": "string"
    },
    "vaccine_type_id": {
      "$ref": "#/components/schemas/IdType"
    }
  },
  "required": [
    "vaccine_type_id",
    "vaccine_type"
  ],
  "type": "object"
},
1031
1041

```

```
        },
        "VariantHLARecord": {
            "properties": {
                "hla": {
                    "type": "string"
                },
                "hla_id": {
                    "$ref": "#/components/schemas/IdType"
                }
            },
            "required": [
                "hla_id",
                "hla"
            ],
            "type": "object"
        },
        "VariantMethodRecord": {
            "properties": {
                "variant_method": {
                    "type": "string"
                },
                "variant_method_id": {
                    "$ref": "#/components/schemas/IdType"
                }
            },
            "required": [
                "variant_method_id",
                "variant_method"
            ],
            "type": "object"
        },
        "VariantMutationTypeRecord": {
            "properties": {
                "mutation_type": {
                    "type": "string"
                },
                "mutation_type_id": {
                    "$ref": "#/components/schemas/IdType"
                }
            },
            "required": [
                "mutation_type_id",
                "mutation_type"
            ],
            "type": "object"
        }
    }
}
```

```

        "type": "object"
    },
    "VariantProteinRecord": {
        "properties": {
            "protein": {
                "type": "string"
            },
            "protein_id": {
                "$ref": "#/components/schemas/IdType"
            }
        },
        "required": [
            "protein_id",
            "protein"
        ],
        "type": "object"
    },
    "VariantRecord": {
        "description": "Record describing an epitope variant",
        "properties": {
            "epitope": {
                "type": "string"
            },
            "epitope_subtypes": {
                "items": {
                    "type": "string"
                },
                "nullable": true,
                "type": "array"
            },
            "methods": {
                "items": {
                    "type": "string"
                },
                "nullable": true,
                "type": "array"
            },
            "mutation_types": {
                "items": {
                    "properties": {
                        "description": {
                            "type": "string"
                        },
                        "mutation_code": {

```

1091

1101

1111

1121

```
    "type": "string"
  },
  "mutation_type": {
    "type": "string"
  },
  "mutation_type_id": {
    "$ref": "#/components/schemas/IdType"
  }
},
"required": [
  "mutation_type_id",
  "mutation_code",
  "mutation_type",
  "description"
],
"type": "object"
},
"type": "array"
},
"mutations": {
  "items": {
    "properties": {
      "epitope_position": {
        "type": "string"
      },
      "hxb2_position": {
        "type": "string"
      },
      "mutation": {
        "maxLength": 1,
        "minLength": 1,
        "type": "string"
      },
      "original": {
        "maxLength": 1,
        "minLength": 1,
        "type": "string"
      }
    },
    "required": [
      "epitope_position",
      "hxb2_position",
      "mutation",
      "original"
    ]
  }
}
```

```

        ],
        "type": "object"
    },
    "type": "array"
},
"note": {
    "nullable": true,
    "type": "string"
},
"variant_epitope": {
    "type": "string"
},
"variant_id": {
    "$ref": "#/components/schemas/IdType"
},
"variant_subtypes": {
    "items": {
        "type": "string"
    },
    "nullable": true,
    "type": "array"
}
},
"required": [
    "epitope",
    "methods",
    "mutation_types",
    "mutations",
    "variant_epitope",
    "variant_id",
    "variant_subtypes"
],
"type": "object"
},
"VariantTable": {
    "description": "The tables which have epitope variants",
    "enum": [
        "ctl",
        "helper"
    ],
    "type": "string"
},
"listBindingTypeResponse": {
    "properties": {

```

```

        "binding_type": {
            "items": {
                "$ref": "#/components/schemas/BindingTypeRecord"
            },
            "type": "array"
        },
        "table": {
            "$ref": "#/components/schemas/Table"
        },
        "timestamp": {
            "$ref": "#/components/schemas/TimeStamp"
        }
    },
    "required": [
        "binding_type",
        "table",
        "timestamp"
    ],
    "type": "object"
},
"listCountryResponse": {
    "properties": {
        "country": {
            "items": {
                "$ref": "#/components/schemas/CountryRecord"
            },
            "type": "array"
        },
        "table": {
            "$ref": "#/components/schemas/Table"
        },
        "timestamp": {
            "$ref": "#/components/schemas/TimeStamp"
        }
    },
    "required": [
        "country",
        "table",
        "timestamp"
    ],
    "type": "object"
},
"listHLAResponse": {
    "properties": {
1221
1231
1241
1251
1261

```

```

        "hla": {
            "items": {
                "$ref": "#/components/schemas/HLARecord"
            },
            "type": "array"
        },
        "table": {
            "$ref": "#/components/schemas/Table"
        },
        "timestamp": {
            "$ref": "#/components/schemas/TimeStamp"
        }
    },
    "required": [
        "hla",
        "table",
        "timestamp"
    ],
    "type": "object"
},
1281
"listImmunogenResponse": {
    "properties": {
        "immunogen": {
            "items": {
                "$ref": "#/components/schemas/ImmunogenRecord"
            },
            "type": "array"
        },
        "table": {
            "$ref": "#/components/schemas/Table"
        },
        "timestamp": {
            "$ref": "#/components/schemas/TimeStamp"
        }
    },
    "required": [
        "immunogen",
        "table",
        "timestamp"
    ],
    "type": "object"
},
1291
"listIsotypeResponse": {
    "properties": {

```

```
        "isotype": {
            "items": {
                "$ref": "#/components/schemas/IsotypeRecord"
            },
            "type": "array"
        },
        "table": {
            "$ref": "#/components/schemas/Table"
        },
        "timestamp": {
            "$ref": "#/components/schemas/TimeStamp"
        }
    },
    "required": [
        "isotype",
        "table",
        "timestamp"
    ],
    "type": "object"
},
"listKeywordResponse": {
    "properties": {
        "keyword": {
            "items": {
                "$ref": "#/components/schemas/KeywordRecord"
            },
            "type": "array"
        },
        "table": {
            "$ref": "#/components/schemas/Table"
        },
        "timestamp": {
            "$ref": "#/components/schemas/TimeStamp"
        }
    },
    "required": [
        "keyword",
        "table",
        "timestamp"
    ],
    "type": "object"
},
"listOutcomeResponse": {
    "properties": {
```

```

    "outcome": {
      "items": {
        "$ref": "#/components/schemas/OutcomeRecord"
      },
      "type": "array"
    },
    "table": {
      "$ref": "#/components/schemas/Table"
    },
    "timestamp": {
      "$ref": "#/components/schemas/TimeStamp"
    }
  },
  "required": [
    "outcome",
    "table",
    "timestamp"
  ],
  "type": "object"
},
"listPatientEthnicityResponse": {
  "properties": {
    "ethnicity": {
      "items": {
        "$ref": "#/components/schemas/PatientEthnicityRecord"
      },
      "type": "array"
    },
    "timestamp": {
      "$ref": "#/components/schemas/TimeStamp"
    }
  },
  "required": [
    "ethnicity",
    "timestamp"
  ],
  "type": "object"
},
"listPatientHLAResponse": {
  "properties": {
    "hla": {
      "items": {
        "$ref": "#/components/schemas/PatientHLARecord"
      },
      "type": "array"
    }
  }
}

```

```
        "type": "array"
    },
    "timestamp": {
        "$ref": "#/components/schemas/TimeStamp"
    }
},
"required": [
    "hla",
    "timestamp"
],
"type": "object"
},
"listPatientInfectionCountryResponse": {
    "properties": {
        "infection_country": {
            "items": {
                "$ref": "#/components/schemas/PatientInfectionCountryRecord"
            },
            "type": "array"
        },
        "timestamp": {
            "$ref": "#/components/schemas/TimeStamp"
        }
    },
    "required": [
        "infection_country",
        "timestamp"
    ],
    "type": "object"
},
"listPatientInfectionYearResponse": {
    "properties": {
        "infection_year": {
            "items": {
                "$ref": "#/components/schemas/PatientInfectionYearRecord"
            },
            "type": "array"
        },
        "timestamp": {
            "$ref": "#/components/schemas/TimeStamp"
        }
    },
    "required": [
        "infection_year",
        "timestamp"
    ]
}
```

```

        "timestamp"
    ],
    "type": "object"
},
"listPatientProgressionResponse": {
    "properties": {
        "progression": {
            "items": {
                "$ref": "#/components/schemas/PatientProgressionRecord"
            },
            "type": "array"
        },
        "timestamp": {
            "$ref": "#/components/schemas/TimeStamp"
        }
    },
    "required": [
        "progression",
        "timestamp"
    ],
    "type": "object"
},
"listPatientRiskFactorResponse": {
    "properties": {
        "risk_factor": {
            "items": {
                "$ref": "#/components/schemas/PatientRiskFactorRecord"
            },
            "type": "array"
        },
        "timestamp": {
            "$ref": "#/components/schemas/TimeStamp"
        }
    },
    "required": [
        "risk_factor",
        "timestamp"
    ],
    "type": "object"
},
"listPatientSexResponse": {
    "properties": {
        "sex": {
            "items": {

```

1441

1451

1461

1471

1481

```
        "$ref": "#/components/schemas/PatientSexRecord"
    },
    "type": "array"
},
"timestamp": {
    "$ref": "#/components/schemas/TimeStamp"
}
},
"required": [
    "sex",
    "timestamp"
],
"type": "object"
},
"listPatientSpeciesResponse": {
    "properties": {
        "species": {
            "items": {
                "$ref": "#/components/schemas/PatientSpeciesRecord"
            },
            "type": "array"
        },
        "timestamp": {
            "$ref": "#/components/schemas/TimeStamp"
        }
    },
    "required": [
        "species",
        "timestamp"
    ],
    "type": "object"
},
"listProteinResponse": {
    "properties": {
        "protein": {
            "items": {
                "$ref": "#/components/schemas/ProteinRecord"
            },
            "type": "array"
        },
        "table": {
            "$ref": "#/components/schemas/Table"
        },
        "timestamp": {
1491
1501
1511
1521
```

```

        "$ref": "#/components/schemas/TimeStamp"
    }
},
"required": [
    "protein",
    "table",
    "timestamp"
],
"type": "object"
},
"listSpeciesResponse": {
    "properties": {
        "species": {
            "items": {
                "$ref": "#/components/schemas/SpeciesRecord"
            },
            "type": "array"
        },
        "table": {
            "$ref": "#/components/schemas/Table"
        },
        "timestamp": {
            "$ref": "#/components/schemas/TimeStamp"
        }
    },
    "required": [
        "species",
        "table",
        "timestamp"
    ],
    "type": "object"
},
"listSubtypeResponse": {
    "properties": {
        "subtype": {
            "items": {
                "$ref": "#/components/schemas/SubtypeRecord"
            },
            "type": "array"
        },
        "table": {
            "$ref": "#/components/schemas/Table"
        },
        "timestamp": {
1531
1541
1551
1561

```

```
        "$ref": "#/components/schemas/TimeStamp"
    },
},
"required": [
    "subtype",
    "table",
    "timestamp"
],
"type": "object"
},
"listVaccineAdjuvantResponse": {
    "properties": {
        "table": {
            "$ref": "#/components/schemas/Table"
        },
        "timestamp": {
            "$ref": "#/components/schemas/TimeStamp"
        },
        "vaccine_adjuvant": {
            "items": {
                "$ref": "#/components/schemas/VaccineAdjuvantRecord"
            },
            "type": "array"
        }
    },
    "required": [
        "vaccine_adjuvant",
        "table",
        "timestamp"
    ],
    "type": "object"
},
"listVaccineComponentResponse": {
    "properties": {
        "table": {
            "$ref": "#/components/schemas/Table"
        },
        "timestamp": {
            "$ref": "#/components/schemas/TimeStamp"
        },
        "vaccine_component": {
            "items": {
                "$ref": "#/components/schemas/VaccineComponentRecord"
            },
            "type": "array"
        }
    }
}
```

```

        "type": "array"
    },
},
"required": [
    "vaccine_component",
    "table",
    "timestamp"
],
"type": "object"
},
"listVaccineStrainResponse": {
    "properties": {
        "table": {
            "$ref": "#/components/schemas/Table"
        },
        "timestamp": {
            "$ref": "#/components/schemas/TimeStamp"
        },
        "vaccine_strain": {
            "items": {
                "$ref": "#/components/schemas/VaccineStrainRecord"
            },
            "type": "array"
        }
    },
    "required": [
        "vaccine_strain",
        "table",
        "timestamp"
    ],
    "type": "object"
},
"listVaccineTypeResponse": {
    "properties": {
        "table": {
            "$ref": "#/components/schemas/Table"
        },
        "timestamp": {
            "$ref": "#/components/schemas/TimeStamp"
        },
        "vaccine_type": {
            "items": {
                "$ref": "#/components/schemas/VaccineTypeRecord"
            },
            "type": "array"
        }
    }
}
1621
1631
1641
1651

```

```
        "type": "array"
    },
},
"required": [
    "vaccine_type",
    "table",
    "timestamp"
],
"type": "object"
},
"listVariantHLAResponse": {
    "properties": {
        "hla": {
            "items": {
                "$ref": "#/components/schemas/VariantHLARecord"
            },
            "type": "array"
        },
        "table": {
            "$ref": "#/components/schemas/Table"
        },
        "timestamp": {
            "$ref": "#/components/schemas/TimeStamp"
        }
    },
    "required": [
        "hla",
        "table",
        "timestamp"
    ],
    "type": "object"
},
"listVariantMethodResponse": {
    "properties": {
        "table": {
            "$ref": "#/components/schemas/Table"
        },
        "timestamp": {
            "$ref": "#/components/schemas/TimeStamp"
        },
        "variant_method": {
            "items": {
                "$ref": "#/components/schemas/VariantMethodRecord"
            },
            "type": "array"
        }
    }
}
```

```
        "type": "array"
    }
},
"required": [
    "variant_method",
    "table",
    "timestamp"
],
"type": "object"
},
"listVariantMutationTypeResponse": {
"properties": {
    "mutation_type": {
        "items": {
            "$ref": "#/components/schemas/VariantMutationTypeRecord"
        },
        "type": "array"
    },
    "table": {
        "$ref": "#/components/schemas/Table"
    },
    "timestamp": {
        "$ref": "#/components/schemas/TimeStamp"
    }
},
"required": [
    "mutation_type",
    "table",
    "timestamp"
],
"type": "object"
},
"listVariantProteinResponse": {
"properties": {
    "protein": {
        "items": {
            "$ref": "#/components/schemas/VariantProteinRecord"
        },
        "type": "array"
    },
    "table": {
        "$ref": "#/components/schemas/Table"
    },
    "timestamp": {
        "$ref": "#/components/schemas/TimeStamp"
    }
},
"required": [
    "protein"
],
"type": "object"
}
```

```

        "$ref": "#/components/schemas/TimeStamp"
    }
},
"required": [
    "protein",
    "table",
    "timestamp"
],
"type": "object"
}
}
},
"info": {
    "contact": {
        "email": "immuno@lanl.gov",
        "name": "LANL HIV Molecular Immunology Database",
        "url": "https://www.hiv.lanl.gov/content/immunology/index.html"
    },
    "termsOfService": "https://www.lanl.gov/resources/web-policies/copyright-legal. ...
...php",
        "title": "HIV Molecular Immunology API",
        "version": "v2.2.1",
        "x-copyright": "Copyright © Triad National Security, LLC",
        "x-mojo": "❤️ mojolicious"
    },
    "openapi": "3.0.3",
    "paths": {
        "/epitope/{table)": {
            "get": {
                "operationId": "getEpitopes",
                "parameters": [
                    {
                        "description": "Which table to search",
                        "in": "path",
                        "name": "table",
                        "required": true,
                        "schema": {
                            "$ref": "#/components/schemas/Table"
                        }
                    },
                    {
                        "description": "Antibody binding type ID",
                        "in": "query",
                        "name": "binding_type",
                    }
                ]
            }
        }
    }
}

```

```

        "schema": {
            "$ref": "#/components/schemas/IdType"
        }
    },
    {
        "description": "Search for epitopes before this DNA location",
        "in": "query",
        "name": "dna_end",
        "schema": {
            "maximum": 12000,
            "minimum": 1,
            "type": "integer"
        }
    },
    {
        "description": "Search for epitopes after this DNA location",
        "in": "query",
        "name": "dna_start",
        "schema": {
            "maximum": 12000,
            "minimum": 1,
            "type": "integer"
        }
    },
    {
        "description": "Search for epitopes before this protein location; ...  
...requires protein",
        "in": "query",
        "name": "end",
        "schema": {
            "maximum": 1200,
            "minimum": 1,
            "type": "integer"
        }
    },
    {
        "description": "Epitope Restricting HLA/MHC ID",
        "in": "query",
        "name": "hla_id",
        "schema": {
            "$ref": "#/components/schemas/IdType"
        }
    },
    {

```

1791

1801

1811

1821

1831

```
        "description": "Epitope ID",
        "in": "query",
        "name": "id",
        "schema": {
          "$ref": "#/components/schemas/IdType"
        }
      },
      {
        "description": "Immunogen ID",
        "in": "query",
        "name": "immunogen",
        "schema": {
          "$ref": "#/components/schemas/IdType"
        }
      },
      {
        "description": "Isotype ID",
        "in": "query",
        "name": "isotype",
        "schema": {
          "$ref": "#/components/schemas/IdType"
        }
      },
      {
        "description": "Epitope keyword ID",
        "in": "query",
        "name": "keyword",
        "schema": {
          "$ref": "#/components/schemas/IdType"
        }
      },
      {
        "description": "Outcome ID",
        "in": "query",
        "name": "outcome",
        "schema": {
          "$ref": "#/components/schemas/IdType"
        }
      },
      {
        "description": "Epitope is from this protein ID",
        "in": "query",
        "name": "protein",
        "schema": {
```

```

        "$ref": "#/components/schemas/IdType"
    }
},
{
    "description": "PubMed ID of epitope references",
1881
    "in": "query",
    "name": "pubmed_id",
    "schema": {
        "$ref": "#/components/schemas/IdType"
    }
},
{
    "description": "Search for epitopes at this protein location; requires ...
...protein",
    "in": "query",
    "name": "spans",
    "schema": {
        "maximum": 1200,
        "minimum": 1,
        "type": "integer"
    }
},
{
    "description": "Immune response observed in this species ID",
    "in": "query",
    "name": "species",
    "schema": {
        "$ref": "#/components/schemas/IdType"
    }
},
{
    "description": "Search for epitopes after this protein location; requires ...
... protein",
    "in": "query",
    "name": "start",
    "schema": {
        "maximum": 1200,
        "minimum": 1,
        "type": "integer"
    }
},
{
    "description": "Virus subtype ID",
    "in": "query",
1901
    "name": "subtype",
    "schema": {
        "maximum": 1200,
        "minimum": 1,
        "type": "integer"
    }
}
]
}

```

```
        "name": "subtype",
        "schema": {
            "$ref": "#/components/schemas/IdType"
        }
    },
{
    "description": "Vaccine adjuvant ID",
    "in": "query",
    "name": "vaccine_adjuvant",
    "schema": {
        "$ref": "#/components/schemas/IdType"
    }
},
{
    "description": "Vaccine component ID",
    "in": "query",
    "name": "vaccine_component",
    "schema": {
        "$ref": "#/components/schemas/IdType"
    }
},
{
    "description": "Vaccine viral strain ID",
    "in": "query",
    "name": "vaccine_strain",
    "schema": {
        "$ref": "#/components/schemas/IdType"
    }
},
{
    "description": "Vaccine type ID",
    "in": "query",
    "name": "vaccine_type",
    "schema": {
        "$ref": "#/components/schemas/IdType"
    }
},
{
    "description": "Author of a reference",
    "in": "query",
    "name": "author",
    "schema": {
        "maxLength": 100,
        "minLength": 2,
    }
}
```

```

        "type": "string"
    }
},
{
    "description": "Citation key of a reference",
    "in": "query",
    "name": "cite",
    "schema": {
        "maxLength": 30,
        "minLength": 6,
        "type": "string"
    }
},
{
    "description": "Epitope sequence",
    "in": "query",
    "name": "epitope",
    "schema": {
        "maxLength": 20,
        "minLength": 6,
        "pattern": "^[A-Za-z]+$",
        "type": "string"
    }
},
{
    "description": "Epitope name",
    "in": "query",
    "name": "epitope_name",
    "schema": {
        "maxLength": 30,
        "minLength": 3,
        "type": "string"
    }
},
{
    "description": "Restricting MHC/HLA of the epitope. T cell only",
    "in": "query",
    "name": "hla",
    "schema": {
        "maxLength": 20,
        "minLength": 2,
        "type": "string"
    }
},
}

```

```

{
  "description": "Name of the monoclonal antibody (mAb)",
  "in": "query",
  "name": "mab_name",
  "schema": {
    "maxLength": 30,
    "minLength": 3,
    "type": "string"
  }
},
{
  "description": "Text in a note",
  "in": "query",
  "name": "note",
  "schema": {
    "maxLength": 30,
    "minLength": 3,
    "type": "string"
  }
},
{
  "description": "Epitope is from this protein",
  "in": "query",
  "name": "protein_name",
  "schema": {
    "maxLength": 30,
    "minLength": 3,
    "type": "string"
  }
},
{
  "description": "How to match epitope sequence",
  "in": "query",
  "name": "epitope_exact",
  "schema": {
    "enum": [
      "embed",
      "exact",
      "fuzzy"
    ],
    "type": "string"
  }
},
{

```

2011

2021

2031

2041

```
2051     "description": "How to match epitope position",
2052     "in": "query",
2053     "name": "range_span",
2054     "schema": {
2055         "enum": [
2056             "overlap",
2057             "embed",
2058             "exact"
2059         ],
2060         "type": "string"
2061     },
2062     {
2063         "description": "How to match epitope DNA position",
2064         "in": "query",
2065         "name": "dna_range_span",
2066         "schema": {
2067             "enum": [
2068                 "overlap",
2069                 "embed",
2070                 "exact"
2071             ],
2072             "type": "string"
2073         }
2074     },
2075     {
2076         "description": "Restrict author search to first authors",
2077         "in": "query",
2078         "name": "author_first",
2079         "schema": {
2080             "nullable": true,
2081             "type": "boolean"
2082         }
2083     },
2084     {
2085         "description": "Restrict author search to last authors",
2086         "in": "query",
2087         "name": "author_last",
2088         "schema": {
2089             "nullable": true,
2090             "type": "boolean"
2091         }
2092     },
2093     {
```

```

    "description": "Show only this 'authors references (Ab only)",
    "in": "query",
    "name": "au_filter",
    "schema": {
        "nullable": true,
        "type": "boolean"
    }
},
{
    "description": "Show only notes containing selected keyword(s) (Ab only) ...",
    "in": "query",
    "name": "kw_filter",
    "schema": {
        "nullable": true,
        "type": "boolean"
    }
},
{
    "description": "Show only notes matching this text (Ab only)",
    "in": "query",
    "name": "note_filter",
    "schema": {
        "nullable": true,
        "type": "boolean"
    }
}
],
"responses": {
    "200": {
        "content": {
            "application/json": {
                "schema": {
                    "$ref": "#/components/schemas/EpitopeResponse"
                }
            }
        },
        "description": "Epitopes"
    },
    "400": {
        "content": {
            "application/json": {
                "schema": {
                    "$ref": "#/components/schemas/DefaultResponse"
                }
            }
        }
    }
}

```

```
        }
    },
},
"description": "Default response."
2141 },
"401": {
"content": {
"application/json": {
"schema": {
"$ref": "#/components/schemas/DefaultResponse"
}
}
},
"description": "Default response."
2151 },
"404": {
"content": {
"application/json": {
"schema": {
"$ref": "#/components/schemas/DefaultResponse"
}
}
},
"description": "Default response."
2161 },
"500": {
"content": {
"application/json": {
"schema": {
"$ref": "#/components/schemas/DefaultResponse"
}
}
},
"description": "Default response."
2171 },
"501": {
"content": {
"application/json": {
"schema": {
"$ref": "#/components/schemas/DefaultResponse"
}
}
},
"description": "Default response."
```

```

2181         }
        },
        "summary": "Finds epitope records in the database"
    }
},
"/list/binding_type/{table}": {
    "get": {
        "operationId": "listBindingType",
        "parameters": [
            {
                "in": "path",
                "name": "table",
                "required": true,
                "schema": {
                    "$ref": "#/components/schemas/AbTable"
                }
            }
        ],
        "responses": {
            "200": {
                "content": {
                    "application/json": {
                        "schema": {
                            "$ref": "#/components/schemas/listBindingTypeResponse"
                        }
                    }
                },
                "description": "Binding types"
            },
            "400": {
                "content": {
                    "application/json": {
                        "schema": {
                            "$ref": "#/components/schemas/DefaultResponse"
                        }
                    }
                },
                "description": "Default response."
            },
            "401": {
                "content": {
                    "application/json": {
                        "schema": {
                            "$ref": "#/components/schemas/DefaultResponse"
                        }
                    }
                }
            }
        }
    }
}
2191
2201
2211
2221

```

```

        }
    },
},
"description": "Default response."
},
"404": {
"content": {
"application/json": {
"schema": {
"$ref": "#/components/schemas/DefaultResponse"
}
}
},
"description": "Default response."
},
"500": {
"content": {
"application/json": {
"schema": {
"$ref": "#/components/schemas/DefaultResponse"
}
}
},
"description": "Default response."
},
"501": {
"content": {
"application/json": {
"schema": {
"$ref": "#/components/schemas/DefaultResponse"
}
}
},
"description": "Default response."
},
"summary": "List binding types in the database"
},
"/list/country/{table)": {
"get": {
"operationId": "listCountry",
"parameters": [
{

```

```
2271     "in": "path",
2272     "name": "table",
2273     "required": true,
2274     "schema": {
2275       "$ref": "#/components/schemas/Table"
2276     }
2277   ],
2278   "responses": {
2279     "200": {
2280       "content": {
2281         "application/json": {
2282           "schema": {
2283             "$ref": "#/components/schemas/listCountryResponse"
2284           }
2285         }
2286       },
2287       "description": "Countries"
2288     },
2289     "400": {
2290       "content": {
2291         "application/json": {
2292           "schema": {
2293             "$ref": "#/components/schemas/DefaultResponse"
2294           }
2295         }
2296       },
2297       "description": "Default response."
2298     },
2299     "401": {
2300       "content": {
2301         "application/json": {
2302           "schema": {
2303             "$ref": "#/components/schemas/DefaultResponse"
2304           }
2305         }
2306       },
2307       "description": "Default response."
2308     },
2309     "404": {
2310       "content": {
2311         "application/json": {
2312           "schema": {
2313             "$ref": "#/components/schemas/DefaultResponse"
2314           }
2315         }
2316       }
2317     }
2318   }
2319 }
```

```

        }
    },
},
"description": "Default response."
},
"500": {
"content": {
"application/json": {
"schema": {
"$ref": "#/components/schemas/DefaultResponse"
}
}
},
"description": "Default response."
},
"501": {
"content": {
"application/json": {
"schema": {
"$ref": "#/components/schemas/DefaultResponse"
}
}
},
"description": "Default response."
}
},
"summary": "List countries in the database"
}
},
2341
"/list/hla/{table)": {
"get": {
"operationId": "listHLA",
"parameters": [
{
"in": "path",
"name": "table",
"required": true,
"schema": {
"$ref": "#/components/schemas/TCellTable"
}
}
],
"responses": {
"200": {

```

```
2361     "content": {
      "application/json": {
        "schema": {
          "$ref": "#/components/schemas/listHLAResponse"
        }
      }
    },
    "description": "HLAs"
  },
  "400": {
    "content": {
      "application/json": {
        "schema": {
          "$ref": "#/components/schemas/DefaultResponse"
        }
      }
    },
    "description": "Default response."
  },
  "401": {
    "content": {
      "application/json": {
        "schema": {
          "$ref": "#/components/schemas/DefaultResponse"
        }
      }
    },
    "description": "Default response."
  },
  "404": {
    "content": {
      "application/json": {
        "schema": {
          "$ref": "#/components/schemas/DefaultResponse"
        }
      }
    },
    "description": "Default response."
  },
  "500": {
    "content": {
      "application/json": {
        "schema": {
          "$ref": "#/components/schemas/DefaultResponse"
        }
      }
    }
  }
}
```

```
        }
    },
},
"description": "Default response."
},
"501": {
"content": {
"application/json": {
"schema": {
"$ref": "#/components/schemas/DefaultResponse"
}
}
},
"description": "Default response."
}
},
"summary": "List restricting HLAs in the database"
}
},
"/list/immunogen/{table)": {
"get": {
"operationId": "listImmunogen",
"parameters": [
{
"in": "path",
"name": "table",
"required": true,
"schema": {
"$ref": "#/components/schemas/Table"
}
}
]
},
"responses": {
"200": {
"content": {
"application/json": {
"schema": {
"$ref": "#/components/schemas/listImmunogenResponse"
}
}
},
"description": "Immunogens"
}
},
"400": {

```

```
"content": {
  "application/json": {
    "schema": {
      "$ref": "#/components/schemas/DefaultResponse"
    }
  }
},
"description": "Default response."
},
"401": {
  "content": {
    "application/json": {
      "schema": {
        "$ref": "#/components/schemas/DefaultResponse"
      }
    }
  },
  "description": "Default response."
},
"404": {
  "content": {
    "application/json": {
      "schema": {
        "$ref": "#/components/schemas/DefaultResponse"
      }
    }
  },
  "description": "Default response."
},
"500": {
  "content": {
    "application/json": {
      "schema": {
        "$ref": "#/components/schemas/DefaultResponse"
      }
    }
  },
  "description": "Default response."
},
"501": {
  "content": {
    "application/json": {
      "schema": {
        "$ref": "#/components/schemas/DefaultResponse"
      }
    }
  }
}
```

```

        }
    }
},
"description": "Default response."
},
"summary": "List immunogens in the database"
},
"/list/isotype/{table}": {
"get": {
"operationId": "listIsotype",
"parameters": [
{
"in": "path",
"name": "table",
"required": true,
"schema": {
"$ref": "#/components/schemas/AbTable"
}
},
],
"responses": {
"200": {
"content": {
"application/json": {
"schema": {
"$ref": "#/components/schemas/listIsotypeResponse"
}
}
},
"description": "Isotypes"
},
"400": {
"content": {
"application/json": {
"schema": {
"$ref": "#/components/schemas/DefaultResponse"
}
}
},
"description": "Default response."
},
"401": {

```

```
"content": {
    "application/json": {
        "schema": {
            "$ref": "#/components/schemas/DefaultResponse"
        }
    },
    "description": "Default response."
},
"404": {
    "content": {
        "application/json": {
            "schema": {
                "$ref": "#/components/schemas/DefaultResponse"
            }
        },
        "description": "Default response."
},
"500": {
    "content": {
        "application/json": {
            "schema": {
                "$ref": "#/components/schemas/DefaultResponse"
            }
        },
        "description": "Default response."
},
"501": {
    "content": {
        "application/json": {
            "schema": {
                "$ref": "#/components/schemas/DefaultResponse"
            }
        },
        "description": "Default response."
},
"summary": "List isotopes in the database"
},
"/list/keyword/{table}": {
```

```

"get": {
  "operationId": "listKeyword",
  "parameters": [
    {
      "in": "path",
      "name": "table",
      "required": true,
      "schema": {
        "$ref": "#/components/schemas/Table"
      }
    }
  ],
  "responses": {
    "200": {
      "content": {
        "application/json": {
          "schema": {
            "$ref": "#/components/schemas/listKeywordResponse"
          }
        }
      },
      "description": "Keywords"
    },
    "400": {
      "content": {
        "application/json": {
          "schema": {
            "$ref": "#/components/schemas/DefaultResponse"
          }
        }
      },
      "description": "Default response."
    },
    "401": {
      "content": {
        "application/json": {
          "schema": {
            "$ref": "#/components/schemas/DefaultResponse"
          }
        }
      },
      "description": "Default response."
    },
    "404": {
      "content": {
        "application/json": {
          "schema": {
            "$ref": "#/components/schemas/DefaultResponse"
          }
        }
      },
      "description": "Default response."
    }
  }
}

```

```

2621     "content": {
2622       "application/json": {
2623         "schema": {
2624           "$ref": "#/components/schemas/DefaultResponse"
2625         }
2626       },
2627       "description": "Default response."
2628     },
2629     "500": {
2630       "content": {
2631         "application/json": {
2632           "schema": {
2633             "$ref": "#/components/schemas/DefaultResponse"
2634           }
2635         },
2636         "description": "Default response."
2637       },
2638       "501": {
2639         "content": {
2640           "application/json": {
2641             "schema": {
2642               "$ref": "#/components/schemas/DefaultResponse"
2643             }
2644           },
2645           "description": "Default response."
2646         },
2647         "summary": "List keywords in the database"
2648       },
2649     },
2650     "/list/outcome/{table)": {
2651       "get": {
2652         "operationId": "listOutcome",
2653         "parameters": [
2654           {
2655             "in": "path",
2656             "name": "table",
2657             "required": true,
2658             "schema": {
2659               "$ref": "#/components/schemas/TCellTable"
2660             }
2661           }
2662         ]
2663       }
2664     }
2665   }
2666 }
```

```
        }
    ],
  "responses": {
    "200": {
      "content": {
        "application/json": {
          "schema": {
            "$ref": "#/components/schemas/listOutcomeResponse"
          }
        }
      },
      "description": "Outcomes"
    },
    "400": {
      "content": {
        "application/json": {
          "schema": {
            "$ref": "#/components/schemas/DefaultResponse"
          }
        }
      },
      "description": "Default response."
    },
    "401": {
      "content": {
        "application/json": {
          "schema": {
            "$ref": "#/components/schemas/DefaultResponse"
          }
        }
      },
      "description": "Default response."
    },
    "404": {
      "content": {
        "application/json": {
          "schema": {
            "$ref": "#/components/schemas/DefaultResponse"
          }
        }
      },
      "description": "Default response."
    },
    "500": {
```

```
    "content": {
      "application/json": {
        "schema": {
          "$ref": "#/components/schemas/DefaultResponse"
        }
      }
    },
    "description": "Default response."
  },
  "501": {
    "content": {
      "application/json": {
        "schema": {
          "$ref": "#/components/schemas/DefaultResponse"
        }
      }
    },
    "description": "Default response."
  }
},
"summary": "List outcomes in the database"
}
},
2731
"/list/protein/{table)": {
  "get": {
    "operationId": "listProtein",
    "parameters": [
      {
        "in": "path",
        "name": "table",
        "required": true,
        "schema": {
          "$ref": "#/components/schemas/Table"
        }
      }
    ],
    "responses": {
      "200": {
        "content": {
          "application/json": {
            "schema": {
              "$ref": "#/components/schemas/listProteinResponse"
            }
          }
        }
      }
    }
  }
},
2741
2751
```

```
        },
        "description": "HXB2 protein"
    },
    "400": {
        "content": {
            "application/json": {
                "schema": {
                    "$ref": "#/components/schemas/DefaultResponse"
                }
            }
        },
        "description": "Default response."
    },
    "401": {
        "content": {
            "application/json": {
                "schema": {
                    "$ref": "#/components/schemas/DefaultResponse"
                }
            }
        },
        "description": "Default response."
    },
    "404": {
        "content": {
            "application/json": {
                "schema": {
                    "$ref": "#/components/schemas/DefaultResponse"
                }
            }
        },
        "description": "Default response."
    },
    "500": {
        "content": {
            "application/json": {
                "schema": {
                    "$ref": "#/components/schemas/DefaultResponse"
                }
            }
        },
        "description": "Default response."
    },
    "501": {
```

```
    "content": {
        "application/json": {
            "schema": {
                "$ref": "#/components/schemas/DefaultResponse"
            }
        }
    },
    "description": "Default response."
}
},
"summary": "List HXB2 proteins in the database"
}
},
2801
"/list/species/{table)": {
    "get": {
        "operationId": "listSpecies",
        "parameters": [
            {
                "in": "path",
                "name": "table",
                "required": true,
                "schema": {
                    "$ref": "#/components/schemas/Table"
                }
            }
        ],
        "responses": {
            "200": {
                "content": {
                    "application/json": {
                        "schema": {
                            "$ref": "#/components/schemas/listSpeciesResponse"
                        }
                    }
                },
                "description": "Species"
            },
            "400": {
                "content": {
                    "application/json": {
                        "schema": {
                            "$ref": "#/components/schemas/DefaultResponse"
                        }
                    }
                }
            }
        }
    }
},
2811
2821
2831
```

```
2841     },
  "description": "Default response."
},
"401": {
  "content": {
    "application/json": {
      "schema": {
        "$ref": "#/components/schemas/DefaultResponse"
      }
    }
  },
  "description": "Default response."
},
"404": {
  "content": {
    "application/json": {
      "schema": {
        "$ref": "#/components/schemas/DefaultResponse"
      }
    }
  },
  "description": "Default response."
},
"500": {
  "content": {
    "application/json": {
      "schema": {
        "$ref": "#/components/schemas/DefaultResponse"
      }
    }
  },
  "description": "Default response."
},
"501": {
  "content": {
    "application/json": {
      "schema": {
        "$ref": "#/components/schemas/DefaultResponse"
      }
    }
  },
  "description": "Default response."
},
"2851
2861
2871
2881
```

```
        "summary": "List species in the database"
    }
},
"/list/subtype/{table}": {
    "get": {
        "operationId": "listSubtype",
        "parameters": [
            {
                "in": "path",
                "name": "table",
                "required": true,
                "schema": {
                    "$ref": "#/components/schemas/Table"
                }
            }
        ],
        "responses": {
            "200": {
                "content": {
                    "application/json": {
                        "schema": {
                            "$ref": "#/components/schemas/listSubtypeResponse"
                        }
                    }
                },
                "description": "Subtypes"
            },
            "400": {
                "content": {
                    "application/json": {
                        "schema": {
                            "$ref": "#/components/schemas/DefaultResponse"
                        }
                    }
                },
                "description": "Default response."
            },
            "401": {
                "content": {
                    "application/json": {
                        "schema": {
                            "$ref": "#/components/schemas/DefaultResponse"
                        }
                    }
                }
            }
        }
    }
}
```

```

        },
        "description": "Default response."
    },
    "404": {
        "content": {
            "application/json": {
                "schema": {
                    "$ref": "#/components/schemas/DefaultResponse"
                }
            }
        },
        "description": "Default response."
    },
    "500": {
        "content": {
            "application/json": {
                "schema": {
                    "$ref": "#/components/schemas/DefaultResponse"
                }
            }
        },
        "description": "Default response."
    },
    "501": {
        "content": {
            "application/json": {
                "schema": {
                    "$ref": "#/components/schemas/DefaultResponse"
                }
            }
        },
        "description": "Default response."
    }
},
{
    "summary": "List subtypes in the database"
}
},
"/list/vaccine_adjuvant/{table)": {
    "get": {
        "operationId": "listVaccineAdjuvant",
        "parameters": [
            {
                "in": "path",
                "name": "table",

```

```
        "required": true,
        "schema": {
            "$ref": "#/components/schemas/Table"
        }
    },
],
"responses": {
    "200": {
        "content": {
            "application/json": {
                "schema": {
                    "$ref": "#/components/schemas/listVaccineAdjuvantResponse"
                }
            }
        },
        "description": "Vaccine adjuvants"
    },
    "400": {
        "content": {
            "application/json": {
                "schema": {
                    "$ref": "#/components/schemas/DefaultResponse"
                }
            }
        },
        "description": "Default response."
    },
    "401": {
        "content": {
            "application/json": {
                "schema": {
                    "$ref": "#/components/schemas/DefaultResponse"
                }
            }
        },
        "description": "Default response."
    },
    "404": {
        "content": {
            "application/json": {
                "schema": {
                    "$ref": "#/components/schemas/DefaultResponse"
                }
            }
        }
    }
}
```

```

        },
        "description": "Default response."
    },
    "500": {
        "content": {
            "application/json": {
                "schema": {
                    "$ref": "#/components/schemas/DefaultResponse"
                }
            }
        },
        "description": "Default response."
    },
    "501": {
        "content": {
            "application/json": {
                "schema": {
                    "$ref": "#/components/schemas/DefaultResponse"
                }
            }
        },
        "description": "Default response."
    }
},
"summary": "List vaccine adjuvants in the database"
}
},
"/list/vaccine_component/{table)": {
    "get": {
        "operationId": "listVaccineComponent",
        "parameters": [
            {
                "in": "path",
                "name": "table",
                "required": true,
                "schema": {
                    "$ref": "#/components/schemas/Table"
                }
            }
        ],
        "responses": {
            "200": {
                "content": {
                    "application/json": {
3051

```

```
3061         "schema": {
3062             "$ref": "#/components/schemas/listVaccineComponentResponse"
3063         }
3064     },
3065     "description": "Vaccine components"
3066 },
3067 "400": {
3068     "content": {
3069         "application/json": {
3070             "schema": {
3071                 "$ref": "#/components/schemas/DefaultResponse"
3072             }
3073         }
3074     },
3075     "description": "Default response."
3076 },
3077 "401": {
3078     "content": {
3079         "application/json": {
3080             "schema": {
3081                 "$ref": "#/components/schemas/DefaultResponse"
3082             }
3083         }
3084     },
3085     "description": "Default response."
3086 },
3087 "404": {
3088     "content": {
3089         "application/json": {
3090             "schema": {
3091                 "$ref": "#/components/schemas/DefaultResponse"
3092             }
3093         }
3094     },
3095     "description": "Default response."
3096 },
3097 "500": {
3098     "content": {
3099         "application/json": {
3100             "schema": {
3101                 "$ref": "#/components/schemas/DefaultResponse"
3102             }
3103         }
3104     }
3105 }
```

```

        },
        "description": "Default response."
    },
    "501": {
        "content": {
            "application/json": {
                "schema": {
                    "$ref": "#/components/schemas/DefaultResponse"
                }
            }
        },
        "description": "Default response."
    }
},
"summary": "List vaccine components in the database"
}
},
3121 "/list/vaccine_strain/{table}": {
    "get": {
        "operationId": "listVaccineStrain",
        "parameters": [
            {
                "in": "path",
                "name": "table",
                "required": true,
                "schema": {
                    "$ref": "#/components/schemas/Table"
                }
            }
        ],
        "responses": {
            "200": {
                "content": {
                    "application/json": {
                        "schema": {
                            "$ref": "#/components/schemas/listVaccineStrainResponse"
                        }
                    }
                },
                "description": "Vaccine strains"
            },
            "400": {
                "content": {
                    "application/json": {
3131
3141

```

```
    "schema": {
        "$ref": "#/components/schemas/DefaultResponse"
    }
},
"description": "Default response."
},
"401": {
    "content": {
        "application/json": {
            "schema": {
                "$ref": "#/components/schemas/DefaultResponse"
            }
        }
    },
    "description": "Default response."
},
"404": {
    "content": {
        "application/json": {
            "schema": {
                "$ref": "#/components/schemas/DefaultResponse"
            }
        }
    },
    "description": "Default response."
},
"500": {
    "content": {
        "application/json": {
            "schema": {
                "$ref": "#/components/schemas/DefaultResponse"
            }
        }
    },
    "description": "Default response."
},
"501": {
    "content": {
        "application/json": {
            "schema": {
                "$ref": "#/components/schemas/DefaultResponse"
            }
        }
    }
}
```

```

        },
        "description": "Default response."
    }
},
"summary": "List vaccine strains in the database"
}
},
"/list/vaccine_type/{table}": {
"get": {
"operationId": "listVaccineType",
"parameters": [
{
"in": "path",
"name": "table",
"required": true,
"schema": {
"$ref": "#/components/schemas/Table"
}
}
],
"responses": {
"200": {
"content": {
"application/json": {
"schema": {
"$ref": "#/components/schemas/listVaccineTypeResponse"
}
}
},
"description": "Vaccine types"
},
"400": {
"content": {
"application/json": {
"schema": {
"$ref": "#/components/schemas/DefaultResponse"
}
}
}
},
"description": "Default response."
},
"401": {
"content": {
"application/json": {

```

3201

3211

3221

3231

```
        "schema": {
            "$ref": "#/components/schemas/DefaultResponse"
        }
    },
    "description": "Default response."
},
"404": {
    "content": {
        "application/json": {
            "schema": {
                "$ref": "#/components/schemas/DefaultResponse"
            }
        }
    },
    "description": "Default response."
},
"500": {
    "content": {
        "application/json": {
            "schema": {
                "$ref": "#/components/schemas/DefaultResponse"
            }
        }
    },
    "description": "Default response."
},
"501": {
    "content": {
        "application/json": {
            "schema": {
                "$ref": "#/components/schemas/DefaultResponse"
            }
        }
    },
    "description": "Default response."
}
},
"summary": "List vaccine types in the database"
},
"/patient": {
    "get": {
        "operationId": "getPatients",
```

```
3281     "parameters": [
      {
        "description": "Patient ID",
        "in": "query",
        "name": "id",
        "schema": {
          "$ref": "#/components/schemas/IdType"
        }
      },
      {
        "description": "Infection year",
        "in": "query",
        "name": "infection_year",
        "schema": {
          "maximum": 2100,
          "minimum": 1967,
          "type": "integer"
        }
      },
      {
        "description": "Patient HLA ID",
        "in": "query",
        "name": "patient_hla_id",
        "schema": {
          "$ref": "#/components/schemas/IdType"
        }
      },
      {
        "description": "Species ID",
        "in": "query",
        "name": "species",
        "schema": {
          "$ref": "#/components/schemas/IdType"
        }
      },
      {
        "description": "Patient ethnicity",
        "in": "query",
        "name": "ethnicity",
        "schema": {
          "maxLength": 100,
          "minLength": 2,
          "type": "string"
        }
      }
```

```
        },
        {
            "description": "Patient note",
            "in": "query",
            "name": "note",
            "schema": {
                "maxLength": 100,
                "minLength": 2,
                "type": "string"
            }
        },
        {
            "description": "Patient code",
            "in": "query",
            "name": "patient_code",
            "schema": {
                "maxLength": 100,
                "minLength": 2,
                "type": "string"
            }
        },
        {
            "description": "Patient sex",
            "in": "query",
            "name": "patient_sex",
            "schema": {
                "maxLength": 10,
                "minLength": 2,
                "type": "string"
            }
        },
        {
            "description": "Patient HIV progression state code",
            "in": "query",
            "name": "progression",
            "schema": {
                "maxLength": 10,
                "minLength": 2,
                "type": "string"
            }
        },
        {
            "description": "Patient HIV risk factor code",
            "in": "query",
            "name": "risk_factor",
            "schema": {
                "maxLength": 10,
                "minLength": 2,
                "type": "string"
            }
        }
    ]
}
```

```

        "name": "risk_factor",
        "schema": {
            "maxLength": 10,
            "minLength": 2,
            "type": "string"
        }
    },
    {
        "description": "Restrict author search to first authors",
        "in": "query",
        "name": "patient_code_exact",
        "schema": {
            "nullable": true,
            "type": "boolean"
        }
    }
],
"responses": {
    "200": {
        "content": {
            "application/json": {
                "schema": {
                    "$ref": "#/components/schemas/PatientResponse"
                }
            }
        },
        "description": "Patients"
    },
    "400": {
        "content": {
            "application/json": {
                "schema": {
                    "$ref": "#/components/schemas/DefaultResponse"
                }
            }
        },
        "description": "Default response."
    },
    "401": {
        "content": {
            "application/json": {
                "schema": {
                    "$ref": "#/components/schemas/DefaultResponse"
                }
            }
        }
    }
}

```

```

        }
    },
    "description": "Default response."
},
"404": {
    "content": {
        "application/json": {
            "schema": {
                "$ref": "#/components/schemas/DefaultResponse"
            }
        }
    },
    "description": "Default response."
},
"500": {
    "content": {
        "application/json": {
            "schema": {
                "$ref": "#/components/schemas/DefaultResponse"
            }
        }
    },
    "description": "Default response."
},
"501": {
    "content": {
        "application/json": {
            "schema": {
                "$ref": "#/components/schemas/DefaultResponse"
            }
        }
    },
    "description": "Default response."
}
},
"summary": "Finds patient records in the database"
}
},
3451 "/patient_list/ethnicity": {
    "get": {
        "operationId": "listPatientEthnicity",
        "responses": {
            "200": {
                "content": {

```

```
        "application/json": {
          "schema": {
            "$ref": "#/components/schemas/listPatientEthnicityResponse"
          }
        }
      },
      "description": "Ethnicity"
    },
    "400": {
      "content": {
        "application/json": {
          "schema": {
            "$ref": "#/components/schemas/DefaultResponse"
          }
        }
      },
      "description": "Default response."
    },
    "401": {
      "content": {
        "application/json": {
          "schema": {
            "$ref": "#/components/schemas/DefaultResponse"
          }
        }
      },
      "description": "Default response."
    },
    "404": {
      "content": {
        "application/json": {
          "schema": {
            "$ref": "#/components/schemas/DefaultResponse"
          }
        }
      },
      "description": "Default response."
    },
    "500": {
      "content": {
        "application/json": {
          "schema": {
            "$ref": "#/components/schemas/DefaultResponse"
          }
        }
      }
    }
  }
}
```

```

        }
    },
    "description": "Default response."
},
"501": {
    "content": {
        "application/json": {
            "schema": {
                "$ref": "#/components/schemas/DefaultResponse"
            }
        }
    },
    "description": "Default response."
}
},
"summary": "List ethnicities in the patient table"
},
"/patient_list/hla": {
    "get": {
        "operationId": "listPatientHLA",
        "responses": {
            "200": {
                "content": {
                    "application/json": {
                        "schema": {
                            "$ref": "#/components/schemas/listPatientHLAResponse"
                        }
                    }
                },
                "description": "HLAs"
            },
            "400": {
                "content": {
                    "application/json": {
                        "schema": {
                            "$ref": "#/components/schemas/DefaultResponse"
                        }
                    }
                },
                "description": "Default response."
            },
            "401": {
                "content": {

```

3501

3521

3531

3541

```

        "application/json": {
            "schema": {
                "$ref": "#/components/schemas/DefaultResponse"
            }
        },
        "description": "Default response."
    },
    "404": {
        "content": {
            "application/json": {
                "schema": {
                    "$ref": "#/components/schemas/DefaultResponse"
                }
            },
            "description": "Default response."
        },
        "500": {
            "content": {
                "application/json": {
                    "schema": {
                        "$ref": "#/components/schemas/DefaultResponse"
                    }
                }
            },
            "description": "Default response."
        },
        "501": {
            "content": {
                "application/json": {
                    "schema": {
                        "$ref": "#/components/schemas/DefaultResponse"
                    }
                }
            },
            "description": "Default response."
        }
    },
    "summary": "List patient HLAs in the database"
},
"/patient_list/infection_country": {
    "get": {

```

```
  "operationId": "listPatientInfectionCountry",
  "responses": {
    "3591"  "200": {
      "content": {
        "application/json": {
          "schema": {
            "$ref": "#/components/schemas/listPatientInfectionCountryResponse"
          }
        },
        "description": "Infection countries"
      },
    "3601"  "400": {
      "content": {
        "application/json": {
          "schema": {
            "$ref": "#/components/schemas/DefaultResponse"
          }
        },
        "description": "Default response."
      },
    "3611"  "401": {
      "content": {
        "application/json": {
          "schema": {
            "$ref": "#/components/schemas/DefaultResponse"
          }
        },
        "description": "Default response."
      },
    "3621"  "404": {
      "content": {
        "application/json": {
          "schema": {
            "$ref": "#/components/schemas/DefaultResponse"
          }
        },
        "description": "Default response."
      },
    "3631"  "500": {
      "content": {
```

```

        "application/json": {
            "schema": {
                "$ref": "#/components/schemas/DefaultResponse"
            }
        }
    },
    "description": "Default response."
},
"501": {
    "content": {
        "application/json": {
            "schema": {
                "$ref": "#/components/schemas/DefaultResponse"
            }
        }
    },
    "description": "Default response."
}
},
"summary": "List infection countries in the database"
}
},
"/patient_list/infection_year": {
    "get": {
        "operationId": "listPatientInfectionYear",
        "responses": {
            "200": {
                "content": {
                    "application/json": {
                        "schema": {
                            "$ref": "#/components/schemas/listPatientInfectionYearResponse"
                        }
                    }
                },
                "description": "Infection countries"
            },
            "400": {
                "content": {
                    "application/json": {
                        "schema": {
                            "$ref": "#/components/schemas/DefaultResponse"
                        }
                    }
                }
            }
        }
    }
}
3661
3671

```

```
    "description": "Default response."
  },
  "401": {
    "content": {
      "application/json": {
        "schema": {
          "$ref": "#/components/schemas/DefaultResponse"
        }
      }
    },
    "description": "Default response."
  },
  "404": {
    "content": {
      "application/json": {
        "schema": {
          "$ref": "#/components/schemas/DefaultResponse"
        }
      }
    },
    "description": "Default response."
  },
  "500": {
    "content": {
      "application/json": {
        "schema": {
          "$ref": "#/components/schemas/DefaultResponse"
        }
      }
    },
    "description": "Default response."
  },
  "501": {
    "content": {
      "application/json": {
        "schema": {
          "$ref": "#/components/schemas/DefaultResponse"
        }
      }
    },
    "description": "Default response."
  }
},
"summary": "List infection years in the database"
```

```

3721     },
3722 },
3723 "/patient_list/progression": {
3724   "get": {
3725     "operationId": "listPatientProgression",
3726     "responses": {
3727       "200": {
3728         "content": {
3729           "application/json": {
3730             "schema": {
3731               "$ref": "#/components/schemas/listPatientProgressionResponse"
3732             }
3733           }
3734         },
3735         "description": "Patient HIV progression"
3736       },
3737       "400": {
3738         "content": {
3739           "application/json": {
3740             "schema": {
3741               "$ref": "#/components/schemas/DefaultResponse"
3742             }
3743           }
3744         },
3745         "description": "Default response."
3746       },
3747       "401": {
3748         "content": {
3749           "application/json": {
3750             "schema": {
3751               "$ref": "#/components/schemas/DefaultResponse"
3752             }
3753           }
3754         },
3755         "description": "Default response."
3756       },
3757       "404": {
3758         "content": {
3759           "application/json": {
3760             "schema": {
3761               "$ref": "#/components/schemas/DefaultResponse"
3762             }
3763           }
3764         },
3765         "description": "Default response."
3766       }
3767     }
3768   }
3769 }

```

```

        "description": "Default response."
    },
    "500": {
        "content": {
            "application/json": {
                "schema": {
                    "$ref": "#/components/schemas/DefaultResponse"
                }
            }
        },
        "description": "Default response."
    },
    "501": {
        "content": {
            "application/json": {
                "schema": {
                    "$ref": "#/components/schemas/DefaultResponse"
                }
            }
        },
        "description": "Default response."
    }
},
"summary": "List patient HIV progression in the database"
}
},
3791 "/patient_list/risk_factor": {
    "get": {
        "operationId": "listPatientRiskFactor",
        "responses": {
            "200": {
                "content": {
                    "application/json": {
                        "schema": {
                            "$ref": "#/components/schemas/listPatientRiskFactorResponse"
                        }
                    }
                }
            },
            "description": "Patient HIV risk factor"
        },
        "400": {
            "content": {
                "application/json": {
                    "schema": {

```

3771

3781

3801

```
        "$ref": "#/components/schemas/DefaultResponse"
    }
},
"description": "Default response."
},
"401": {
"content": {
"application/json": {
"schema": {
"$ref": "#/components/schemas/DefaultResponse"
}
}
},
"description": "Default response."
},
"404": {
"content": {
"application/json": {
"schema": {
"$ref": "#/components/schemas/DefaultResponse"
}
}
},
"description": "Default response."
},
"500": {
"content": {
"application/json": {
"schema": {
"$ref": "#/components/schemas/DefaultResponse"
}
}
},
"description": "Default response."
},
"501": {
"content": {
"application/json": {
"schema": {
"$ref": "#/components/schemas/DefaultResponse"
}
}
},
}
},
3851
```

```
        "description": "Default response."
    },
},
"summary": "List patient HIV risk factor in the database"
},
"/patient_list/sex": {
"get": {
"operationId": "listPatientSex",
"responses": {
"200": {
"content": {
"application/json": {
"schema": {
"$ref": "#/components/schemas/listPatientSexResponse"
}
}
},
"description": "Sex"
},
"400": {
"content": {
"application/json": {
"schema": {
"$ref": "#/components/schemas/DefaultResponse"
}
}
},
"description": "Default response."
},
"401": {
"content": {
"application/json": {
"schema": {
"$ref": "#/components/schemas/DefaultResponse"
}
}
},
"description": "Default response."
},
"404": {
"content": {
"application/json": {
"schema": {

```

```

        "$ref": "#/components/schemas/DefaultResponse"
    }
}
},
"description": "Default response."
},
"500": {
    "content": {
        "application/json": {
            "schema": {
                "$ref": "#/components/schemas/DefaultResponse"
            }
        }
    },
    "description": "Default response."
},
"501": {
    "content": {
        "application/json": {
            "schema": {
                "$ref": "#/components/schemas/DefaultResponse"
            }
        }
    },
    "description": "Default response."
}
},
"summary": "List sexes in the patient table"
}
},
"/patient_list/species": {
    "get": {
        "operationId": "listPatientSpecies",
        "responses": {
            "200": {
                "content": {
                    "application/json": {
                        "schema": {
                            "$ref": "#/components/schemas/listPatientSpeciesResponse"
                        }
                    }
                },
                "description": "Species"
            }
        }
    }
}

```

```
3941     "400": {
        "content": {
            "application/json": {
                "schema": {
                    "$ref": "#/components/schemas/DefaultResponse"
                }
            },
            "description": "Default response."
        },
    },
3951     "401": {
        "content": {
            "application/json": {
                "schema": {
                    "$ref": "#/components/schemas/DefaultResponse"
                }
            },
            "description": "Default response."
        },
    },
3961     "404": {
        "content": {
            "application/json": {
                "schema": {
                    "$ref": "#/components/schemas/DefaultResponse"
                }
            },
            "description": "Default response."
        },
    },
3971     "500": {
        "content": {
            "application/json": {
                "schema": {
                    "$ref": "#/components/schemas/DefaultResponse"
                }
            },
            "description": "Default response."
        },
    },
3981     "501": {
        "content": {
            "application/json": {
                "schema": {

```

```
        "$ref": "#/components/schemas/DefaultResponse"
    }
}
},
"description": "Default response."
}
},
"summary": "List species in the patient table"
}
},
"/variant/{table}": {
"get": {
"operationId": "getVariants",
"parameters": [
{
"description": "Which table to search",
"in": "path",
"name": "table",
"required": true,
"schema": {
"$ref": "#/components/schemas/VariantTable"
}
},
{
"description": "Restrict variants to matching mutation type",
"in": "query",
"name": "mutation_type_filter",
"schema": {
"nullable": true,
"type": "boolean"
}
},
{
"description": "Restrict variants to matching variant ID",
"in": "query",
"name": "variant_id_filter",
"schema": {
"nullable": true,
"type": "boolean"
}
},
{
"description": "Restrict variants to matching variant method",
"in": "query",

```

```

        "name": "variant_method_filter",
        "schema": {
          "nullable": true,
          "type": "boolean"
        }
      },
      {
        "description": "Search for epitopes before this protein location; ...",
        "in": "query",
        "name": "end",
        "schema": {
          "maximum": 1200,
          "minimum": 1,
          "type": "integer"
        }
      },
      {
        "description": "Epitope ID",
        "in": "query",
        "name": "epitope_id",
        "schema": {
          "$ref": "#/components/schemas/IdType"
        }
      },
      {
        "description": "Variant mutation type ID",
        "in": "query",
        "name": "mutation_type_id",
        "schema": {
          "$ref": "#/components/schemas/IdType"
        }
      },
      {
        "description": "Epitope is from this protein ID",
        "in": "query",
        "name": "protein",
        "schema": {
          "$ref": "#/components/schemas/IdType"
        }
      },
      {
        "description": "Search for epitopes at this protein location; requires ...",
        "in": "query",
        "name": "protein",
        "schema": {
          "$ref": "#/components/schemas/IdType"
        }
      }
    ]
  }
}

```

```

4071     "in": "query",
        "name": "spans",
        "schema": {
            "maximum": 1200,
            "minimum": 1,
            "type": "integer"
        }
    },
{
    "description": "Search for epitopes after this protein location; requires ...
... protein",
4081        "in": "query",
        "name": "start",
        "schema": {
            "maximum": 1200,
            "minimum": 1,
            "type": "integer"
        }
    },
{
    "description": "Variant ID",
4091        "in": "query",
        "name": "variant_id",
        "schema": {
            "$ref": "#/components/schemas/IdType"
        }
    },
{
    "description": "Search for variants with this variant method ID",
        "in": "query",
        "name": "variant_method_id",
        "schema": {
            "$ref": "#/components/schemas/IdType"
        }
    },
{
    "description": "Citation key of a reference",
        "in": "query",
        "name": "cite",
        "schema": {
            "maxLength": 30,
            "minLength": 6,
            "type": "string"
        }
}

```

```
        },
        {
            "description": "Epitope or variant sequence",
            "in": "query",
            "name": "epitope",
            "schema": {
                "maxLength": 20,
                "minLength": 6,
                "pattern": "^[A-Za-z]+$",
                "type": "string"
            }
        },
        {
            "description": "Epitope is from this protein",
            "in": "query",
            "name": "protein_name",
            "schema": {
                "maxLength": 30,
                "minLength": 3,
                "type": "string"
            }
        },
        {
            "description": "How to match epitope sequence",
            "in": "query",
            "name": "epitope_exact",
            "schema": {
                "enum": [
                    "embed",
                    "exact",
                    "fuzzy"
                ],
                "type": "string"
            }
        },
        {
            "description": "How to match epitope position",
            "in": "query",
            "name": "range_span",
            "schema": {
                "enum": [
                    "overlap",
                    "embed",
                    "exact"
                ]
            }
        }
    ]
}
```

```

        ],
        "type": "string"
    }
}
],
"responses": {
    "200": {
        "content": {
            "application/json": {
                "schema": {
                    "$ref": "#/components/schemas/EpitopeResponse"
                }
            }
        },
        "description": "Epitopes"
    },
    "400": {
        "content": {
            "application/json": {
                "schema": {
                    "$ref": "#/components/schemas/DefaultResponse"
                }
            }
        },
        "description": "Default response."
    },
    "401": {
        "content": {
            "application/json": {
                "schema": {
                    "$ref": "#/components/schemas/DefaultResponse"
                }
            }
        },
        "description": "Default response."
    },
    "404": {
        "content": {
            "application/json": {
                "schema": {
                    "$ref": "#/components/schemas/DefaultResponse"
                }
            }
        },
        "description": "Default response."
    }
}

```

```

        "description": "Default response."
    },
    "500": {
        "content": {
            "application/json": {
                "schema": {
                    "$ref": "#/components/schemas/DefaultResponse"
                }
            }
        },
        "description": "Default response."
    },
    "501": {
        "content": {
            "application/json": {
                "schema": {
                    "$ref": "#/components/schemas/DefaultResponse"
                }
            }
        },
        "description": "Default response."
    }
},
"summary": "Finds variant epitope records in the database"
}
},
"/variant_list/hla/{table)": {
    "get": {
        "operationId": "listVariantHLA",
        "parameters": [
            {
                "in": "path",
                "name": "table",
                "required": true,
                "schema": {
                    "$ref": "#/components/schemas/VariantTable"
                }
            }
        ],
        "responses": {
            "200": {
                "content": {
                    "application/json": {
                        "schema": {

```

4211

4221

4231

4241

```
        "$ref": "#/components/schemas/listVariantHLAResponse"
    }
}
},
"description": "HLAs"
},
4251
"400": {
"content": {
"application/json": {
"schema": {
"$ref": "#/components/schemas/DefaultResponse"
}
}
},
"description": "Default response."
},
4261
"401": {
"content": {
"application/json": {
"schema": {
"$ref": "#/components/schemas/DefaultResponse"
}
}
},
"description": "Default response."
},
4271
"404": {
"content": {
"application/json": {
"schema": {
"$ref": "#/components/schemas/DefaultResponse"
}
}
},
"description": "Default response."
},
4281
"500": {
"content": {
"application/json": {
"schema": {
"$ref": "#/components/schemas/DefaultResponse"
}
}
},
}
```

```
        "description": "Default response."
    },
    "501": {
        "content": {
            "application/json": {
                "schema": {
                    "$ref": "#/components/schemas/DefaultResponse"
                }
            },
            "description": "Default response."
        }
    },
    "summary": "List restricting HLAs in the database"
}
},
"/variant_list/method/{table)": {
    "get": {
        "operationId": "listVariantMethod",
        "parameters": [
            {
                "in": "path",
                "name": "table",
                "required": true,
                "schema": {
                    "$ref": "#/components/schemas/VariantTable"
                }
            }
        ],
        "responses": {
            "200": {
                "content": {
                    "application/json": {
                        "schema": {
                            "$ref": "#/components/schemas/listVariantMethodResponse"
                        }
                    }
                },
                "description": "variant method"
            },
            "400": {
                "content": {
                    "application/json": {
                        "schema": {

```

```

        "$ref": "#/components/schemas/DefaultResponse"
    }
}
},
"description": "Default response."
},
"401": {
    "content": {
        "application/json": {
            "schema": {
                "$ref": "#/components/schemas/DefaultResponse"
            }
        }
    },
    "description": "Default response."
},
"404": {
    "content": {
        "application/json": {
            "schema": {
                "$ref": "#/components/schemas/DefaultResponse"
            }
        }
    },
    "description": "Default response."
},
"500": {
    "content": {
        "application/json": {
            "schema": {
                "$ref": "#/components/schemas/DefaultResponse"
            }
        }
    },
    "description": "Default response."
},
"501": {
    "content": {
        "application/json": {
            "schema": {
                "$ref": "#/components/schemas/DefaultResponse"
            }
        }
    },
}

```

4341
4351
4361
4371

```
        "description": "Default response."
    },
},
"summary": "List variant methods in the database"
},
"/variant_list/mutation_type/{table}": {
"get": {
"operationId": "listVariantMutationType",
"parameters": [
{
"in": "path",
"name": "table",
"required": true,
"schema": {
"$ref": "#/components/schemas/VariantTable"
}
}
],
"responses": {
"200": {
"content": {
"application/json": {
"schema": {
"$ref": "#/components/schemas/listVariantMutationTypeResponse"
}
}
},
"description": "v"
},
"400": {
"content": {
"application/json": {
"schema": {
"$ref": "#/components/schemas/DefaultResponse"
}
}
}
},
"description": "Default response."
},
"401": {
"content": {
"application/json": {
"schema": {

```

```

        "$ref": "#/components/schemas/DefaultResponse"
    }
}
},
"description": "Default response."
},
"404": {
    "content": {
        "application/json": {
            "schema": {
                "$ref": "#/components/schemas/DefaultResponse"
            }
        }
    },
    "description": "Default response."
},
"500": {
    "content": {
        "application/json": {
            "schema": {
                "$ref": "#/components/schemas/DefaultResponse"
            }
        }
    },
    "description": "Default response."
},
"501": {
    "content": {
        "application/json": {
            "schema": {
                "$ref": "#/components/schemas/DefaultResponse"
            }
        }
    },
    "description": "Default response."
}
},
"summary": "List mutation types in the database"
},
},
"/variant_list/protein/{table)": {
    "get": {
        "operationId": "listVariantProtein",
        "parameters": [

```

4431

4441

4451

4461

```
{  
    "in": "path",  
    "name": "table",  
    "required": true,  
    "schema": {  
        "$ref": "#/components/schemas/VariantTable"  
    }  
},  
]  
,  
"responses": {  
    "200": {  
        "content": {  
            "application/json": {  
                "schema": {  
                    "$ref": "#/components/schemas/listVariantProteinResponse"  
                }  
            }  
        },  
        "description": "HXB2 protein"  
    },  
    "400": {  
        "content": {  
            "application/json": {  
                "schema": {  
                    "$ref": "#/components/schemas/DefaultResponse"  
                }  
            }  
        },  
        "description": "Default response."  
    },  
    "401": {  
        "content": {  
            "application/json": {  
                "schema": {  
                    "$ref": "#/components/schemas/DefaultResponse"  
                }  
            }  
        },  
        "description": "Default response."  
    },  
    "404": {  
        "content": {  
            "application/json": {  
                "schema": {  
                    "$ref": "#/components/schemas/DefaultResponse"  
                }  
            }  
        },  
        "description": "Default response."  
    }  
},  
"4471": {  
    "content": {  
        "application/json": {  
            "schema": {  
                "$ref": "#/components/schemas/VariantTable"  
            }  
        }  
    },  
    "description": "VariantTable response."  
},  
"4481": {  
    "content": {  
        "application/json": {  
            "schema": {  
                "$ref": "#/components/schemas/listVariantProteinResponse"  
            }  
        }  
    },  
    "description": "listVariantProteinResponse response."  
},  
"4491": {  
    "content": {  
        "application/json": {  
            "schema": {  
                "$ref": "#/components/schemas/DefaultResponse"  
            }  
        }  
    },  
    "description": "DefaultResponse response."  
},  
"4501": {  
    "content": {  
        "application/json": {  
            "schema": {  
                "$ref": "#/components/schemas/DefaultResponse"  
            }  
        }  
    },  
    "description": "DefaultResponse response."  
}
```

```
        "$ref": "#/components/schemas/DefaultResponse"
    }
},
},
"description": "Default response."
},
"500": {
"content": {
"application/json": {
"schema": {
"$ref": "#/components/schemas/DefaultResponse"
}
}
},
"description": "Default response."
},
"501": {
"content": {
"application/json": {
"schema": {
"$ref": "#/components/schemas/DefaultResponse"
}
}
},
"description": "Default response."
}
},
"summary": "List HXB2 proteins in the database"
}
}
},
"servers": [
{
"url": "http://127.0.0.1:33159/api/v2"
}
]
}
```

B

Changes

- v 2.2.1 2022-10-27
 - No API changes
 - Search links in menu use mojo search
 - Tweaks to test suite
- v2.2.0 2022-07-27
 - Add help link to search pages
 - Add `spans` and `protein_name` parameter to variant search pages and API.
- v2.0.0 2022-06-29
 - no API changes
 - update version for production release
- v 1.9.4 2022-06-07
 - no API changes
 - reorder variant CSV columns
- v1.9.3 2022-05-15
 - no API changes
 - CSV output for variants
- v1.9.2 2022-05-05
 - no API changes
 - documentation updates
- v1.9.1 2022-03-25
 - add API endpoints for variant lists
- v1.9.0 2022-03-10
 - Breaking change: add ‘epitope/variant/mutations_types’ to OpenAPI schema

- v1.5.2 2022-03-07
 - API and search for variants
 - add `epitope/total_variant_count` to OpenAPI schema
- v1.4.0 2022-02-02
 - no API changes
 - update version for production release
- v 1.3.5 2021-11-03
 - no API changes
 - minor changes to help text
 - convert `<cite>` tags in notes to internal links
- v1.3.4 2021-10-12
 - no API changes
 - less invalid HTML—most remaining errors are DB content
 - update search form
 - “restricting HLA”
- v1.3.3 2021-09-10
 - no API changes
 - refactor API spec generation
 - update help text
- v1.3.2 2021-08-30
 - no API changes
 - implement patient search help links
- v1.3.1 2021-08-18
 - no API changes
 - implement help links
- v1.3.0 2021-08
 - no API changes
 - import search help from legacy search
- v1.2.0 2021-08-10
 - no API changes
 - update version for production release
- v1.1.3 2021-08-04
 - no API changes
 - add links to download search results as JSON or CSV.
- v1.1.2 2021-08-03

- no API changes
- generate correct HTML
- update CSV output format
- v1.1.1 2021-06-16
 - no API changes
 - CSV export of patients
- v1.1.0 2021-06-09
 - no API changes
 - CSV export of epitopes
- v1.0.3 2021-07-22
 - no API changes
 - validate HTML
- v1.0.2 2021-04-28
 - no API changes
 - disconnect from PG after each request
 - create changelog
- v1.0.1 2021-04-22
 - no API changes
 - link to patient search from menu bar
- v1.0.0 2021-03-16
 - Initial public release